

STIC-Biotech/ChemLib

85118

From: Kallis, Russell
Sent: Friday, January 24, 2003 12:34 PM
To: STIC-Biotech/ChemLib
Subject: sequence search request

Hey there!

Sequence search request

Russ Kallis
79117
AU 1638
room 9D06
phone 305-5417
mail CM1 9 E12

case 09/807867

OLIGO search of SEQ ID NO: 1 vs the nucleotide database

SEQ ID NO: 2 vs the protein database

cheers,
Russ

CHFE

Point of Contact:
Susan Hanley
Technical Info. Specialist
CM1 6B05 Tel: 305-4053

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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WEST[Help](#)[Logout](#)[Interrupt](#)[Main Menu](#)[Search Form](#)[Posting Counts](#)[Show S Numbers](#)[Edit S Numbers](#)[Preferences](#)[Cases](#)**Search Results -**

Terms	Documents
L6 and carotenoid.ab.	19

Database: US Patents Full-Text Database ▲
US Pre-Grant Publication Full-Text Database
JPO Abstracts Database
EPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins ▼

Search:

L7

[Refine Search](#)[Recall Text](#)[Clear](#)**Search History**DATE: Thursday, February 20, 2003 [Printable Copy](#) [Create Case](#)**Set Name Query**

side by side

Hit Count Set Name

result set

DB=USPT,DWPI; PLUR=YES; OP=OR

<u>L7</u>	L6 and carotenoid.ab.	19	<u>L7</u>
<u>L6</u>	modification and carotenoid and biosynthesis and pathway	176	<u>L6</u>
<u>L5</u>	TOCB	1	<u>L5</u>
<u>L4</u>	TOCB and carotenoid	0	<u>L4</u>
<u>L3</u>	L2 and terminal and oxidase	1	<u>L3</u>
<u>L2</u>	L1 and carotenoid.ab.	55	<u>L2</u>
<u>L1</u>	carotenoid and biosynthesis and plant	296	<u>L1</u>

END OF SEARCH HISTORY

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NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2	Apr 08	"Ask CAS" for self-help around the clock
NEWS	3	Apr 09	BEILSTEIN: Reload and Implementation of a New Subject Area
NEWS	4	Apr 09	ZDB will be removed from STN
NEWS	5	Apr 19	US Patent Applications available in IFICDB, IFIPAT, and IFIUDB
NEWS	6	Apr 22	Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
NEWS	7	Apr 22	BIOSIS Gene Names now available in TOXCENTER
NEWS	8	Apr 22	Federal Research in Progress (FEDRIP) now available
NEWS	9	Jun 03	New e-mail delivery for search results now available
NEWS	10	Jun 10	MEDLINE Reload
NEWS	11	Jun 10	PCTFULL has been reloaded
NEWS	12	Jul 02	FOREGE no longer contains STANDARDS file segment
NEWS	13	Jul 22	USAN to be reloaded July 28, 2002; saved answer sets no longer valid
NEWS	14	Jul 29	Enhanced polymer searching in REGISTRY
NEWS	15	Jul 30	NETFIRST to be removed from STN
NEWS	16	Aug 08	CANCERLIT reload
NEWS	17	Aug 08	PHARMAMarketLetter(PHARMAML) - new on STN
NEWS	18	Aug 08	NTIS has been reloaded and enhanced
NEWS	19	Aug 19	Aquatic Toxicity Information Retrieval (AQUIRE) now available on STN
NEWS	20	Aug 19	IFIPAT, IFICDB, and IFIUDB have been reloaded
NEWS	21	Aug 19	The MEDLINE file segment of TOXCENTER has been reloaded
NEWS	22	Aug 26	Sequence searching in REGISTRY enhanced
NEWS	23	Sep 03	JAPIO has been reloaded and enhanced
NEWS	24	Sep 16	Experimental properties added to the REGISTRY file
NEWS	25	Sep 16	CA Section Thesaurus available in CAPLUS and CA
NEWS	26	Oct 01	CASREACT Enriched with Reactions from 1907 to 1985
NEWS	27	Oct 21	EVENTLINE has been reloaded
NEWS	28	Oct 24	BEILSTEIN adds new search fields
NEWS	29	Oct 24	Nutraceuticals International (NUTRACEUT) now available on STN
NEWS	30	Oct 25	MEDLINE SDI run of October 8, 2002
NEWS	31	Nov 18	DKILIT has been renamed APOLLIT
NEWS	32	Nov 25	More calculated properties added to REGISTRY
NEWS	33	Dec 02	TIBKAT will be removed from STN
NEWS	34	Dec 04	CSA files on STN
NEWS	35	Dec 17	PCTFULL now covers WP/PCT Applications from 1978 to date
NEWS	36	Dec 17	TOXCENTER enhanced with additional content
NEWS	37	Dec 17	Adis Clinical Trials Insight now available on STN
NEWS	38	Dec 30	ISMEC no longer available

NEWS 39 Jan 13 Indexing added to some pre-1967 records in CA/CAPLUS
 NEWS 40 Jan 21 NUTRACEUT offering one free connect hour in February 2003
 NEWS 41 Jan 21 PHARMAML offering one free connect hour in February 2003
 NEWS 42 Jan 29 Simultaneous left and right truncation added to COMPENDEX,
 ENERGY, INSPEC
 NEWS 43 Feb 13 CANCERLIT is no longer being updated

NEWS EXPRESS January 6 CURRENT WINDOWS VERSION IS V6.01a,
 CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
 AND CURRENT DISCOVER FILE IS DATED 01 OCTOBER 2002
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FULL ESTIMATED COST	0.21	0.21

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=> s TOCB and carotenoid

L1 0 TOCB AND CAROTENOID

=> s carotenoid(w)biosynthes? and rate(w)limiting

L2 8 CAROTENOID(W) BIOSYNTHES? AND RATE(W) LIMITING

=> duplicate remove l2

DUPLICATE PREFERENCE IS 'BIOSIS, EMBASE, CAPLUS'

KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L2

L3 4 DUPLICATE REMOVE L2 (4 DUPLICATES REMOVED)

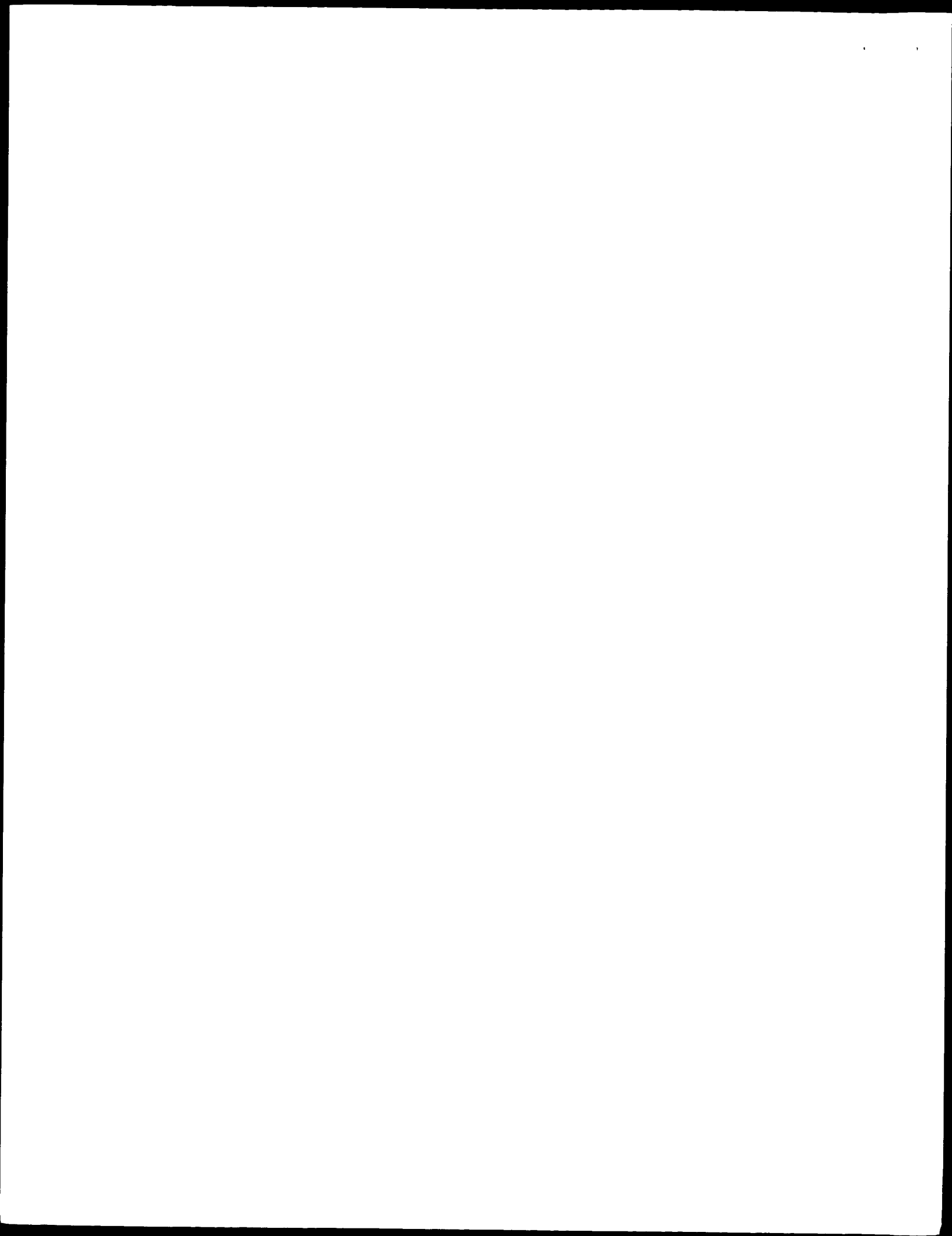
=> d 13 1-4

L3 ANSWER 1 OF 4 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
AN 94252943 EMBASE
DN 1994252943
TI Eubacteria show their true colors: Genetics of carotenoid pigment biosynthesis from microbes to plants.
AU Armstrong G.A.
CS Department of Plant Genetics, Institute for Plant Sciences, Swiss Federal Technology Institute, CH-8092 Zurich, Switzerland
SO Journal of Bacteriology, (1994) 176/16 (4795-4802).
ISSN: 0021-9193 CODEN: JOBAAY
CY United States
DT Journal; (Short Survey)
FS 004 Microbiology
LA English
SL English

L3 ANSWER 2 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
AN 1993:432359 BIOSIS
DN PREV199396086984
TI Molecular and biochemical characterization of herbicide-resistant mutants of cyanobacteria reveals that phytoene desaturation is a ***rate*** -
limiting step in ***carotenoid*** ***biosynthesis*** .
AU Chamovitz, Daniel; Sandmann, Gerhard; Hirschberg, Joseph (1)
CS (1) Dep. Genetics, Hebrew Univ. Jerusalem, Jerusalem 91904 Israel
SO Journal of Biological Chemistry, (1993) Vol. 268, No. 23, pp. 17348-17353.
ISSN: 0021-9258.
DT Article
LA English

L3 ANSWER 3 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2
AN 1993:499191 BIOSIS
DN PREV199396123198
TI Molecular cloning and sequence analysis of the crtB gene of Thermus thermophilus HB27, an extreme thermophile producing carotenoid pigments.
AU Hoshino, Takayuki (1); Fujii, Ryouji; Nakahara, Tadaatsu
CS (1) Inst. Applied Biochem., Univ. Tsukuba, Tsukuba, Ibaraki 305 Japan
SO Applied and Environmental Microbiology, (1993) Vol. 59, No. 9, pp. 3150-3153.
ISSN: 0099-2240.
DT Article
LA English

L3 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2003 ACS
AN 1994:209642 CAPLUS
DN 120:209642
TI Functional expression of the Erwinia uredovora ***carotenoid***
biosynthesis gene crtI in transgenic plants showing an increase
of .beta.-carotene biosynthesis activity and resistance to the bleaching herbicide norflurazon
AU Misawa, Norihiko; Yamano, Shigeyuki; Linden, Hartmut; de Felipe, Maria R.; Lucas, Mercedes; Ikenaga, Hiroshi; Sandmann, Gerhard
CS Cent. Lab. Key Technol., Kirin Brew. Co., Ltd, Yokohama, 236, Japan



SO Plant Journal (1993), 4(5), 833-40
CODEN: PLJUED; ISSN: 0960-7412
DT Journal
LA English

=> FIL STNGUIDE

COST IN U.S. DOLLARS

SINCE FILE

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FULL ESTIMATED COST

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AND TECHNOLOGY CORPORATION, AND FACHINFORMATIONSZENTRUM KARLSRUHE

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LAST RELOADED: Feb 14, 2003 (20030214/UP).

=> file agricola biosis embase caplus

COST IN U.S. DOLLARS

SINCE FILE

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FULL ESTIMATED COST

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FILE 'AGRICOLA' ENTERED AT 18:26:27 ON 20 FEB 2003

FILE 'BIOSIS' ENTERED AT 18:26:27 ON 20 FEB 2003

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FILE 'EMBASE' ENTERED AT 18:26:27 ON 20 FEB 2003

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=> s carotenoid(w)biosynthes? and plant(w)transform?

L4 7 CAROTENOID(W) BIOSYNTHES? AND PLANT(W) TRANSFORM?

=> duplicate remove l4

DUPLICATE PREFERENCE IS 'BIOSIS, EMBASE, CAPLUS'

KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L4

L5 4 DUPLICATE REMOVE L4 (3 DUPLICATES REMOVED)

=> d l5 1-4

L5 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2003 ACS

AN 2002:963266 CAPLUS

TI Stimulation of carotenoid metabolism in arbuscular mycorrhizal roots

AU Fester, Thomas; Schmidt, Diana; Lohse, Swanhild; Walter, Michael H.;
Giuliano, Giovanni; Bramley, Peter M.; Fraser, Paul D.; Hause, Bettina;
Strack, Dieter

CS Leibniz-Institut fur Pflanzenbiochemie, Abteilung Sekundarstoffwechsel,
Halle/Saale, 06120, Germany

SO Planta (2002), 216(1), 148-154

CODEN: PLANAB; ISSN: 0032-0935

PB Springer-Verlag

DT Journal

LA English

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 2 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1

AN 2001:37726 BIOSIS

DN PREV200100037726

TI The chloroplast and leaf developmental mutant, pale cress, exhibits light-conditional severity and symptoms characteristic of its ABA deficiency.

AU Holding, David R. (1); Springer, Patricia S.; Coomber, Shirley A.

CS (1) Department of Botany and Plant Sciences, University of California, Riverside, CA, 92521: dholding@ucr.ac1.ucr.edu USA

SO Annals of Botany (London), (November, 2000) Vol. 86, No. 5, pp. 953-962. print.

ISSN: 0305-7364.

DT Article

LA English

SL English

L5 ANSWER 3 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2

AN 2001:49727 BIOSIS

DN PREV200100049727

TI Identification of a novel gene coding for neoxanthin synthase from Solanum tuberosum.

AU Al-Babili, Salim; Hugueney, Philippe; Schledz, Michael; Welsch, Ralf;

Frohnmeier, Hanns; Laule, Oliver; Beyer, Peter (1)

CS (1) Center for Applied Biosciences, University of Freiburg, Schaeenzlestr. 1, D-79104, Freiburg: beyer@uni-freiburg.de Germany

SO FEBS Letters, (24 November, 2000) Vol. 485, No. 2-3, pp. 168-172. print. ISSN: 0014-5793.

DT Article

LA English

SL English

L5 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2003 ACS

AN 1995:999495 CAPLUS

DN 124:48378

TI Studies on ***carotenoid*** ***biosynthesis*** using the methods of natural products chemistry, molecular biology, and metabolic engineering

AU Misawa, Norihiko

CS Cent. Lab. Key Technol., Kirin Brew. Co., Ltd., Yokohama, 236, Japan

SO Nippon Nogei Kagaku Kaishi (1995), 69(12), 1567-72

CODEN: NNKKAA; ISSN: 0002-1407

DT Journal; General Review

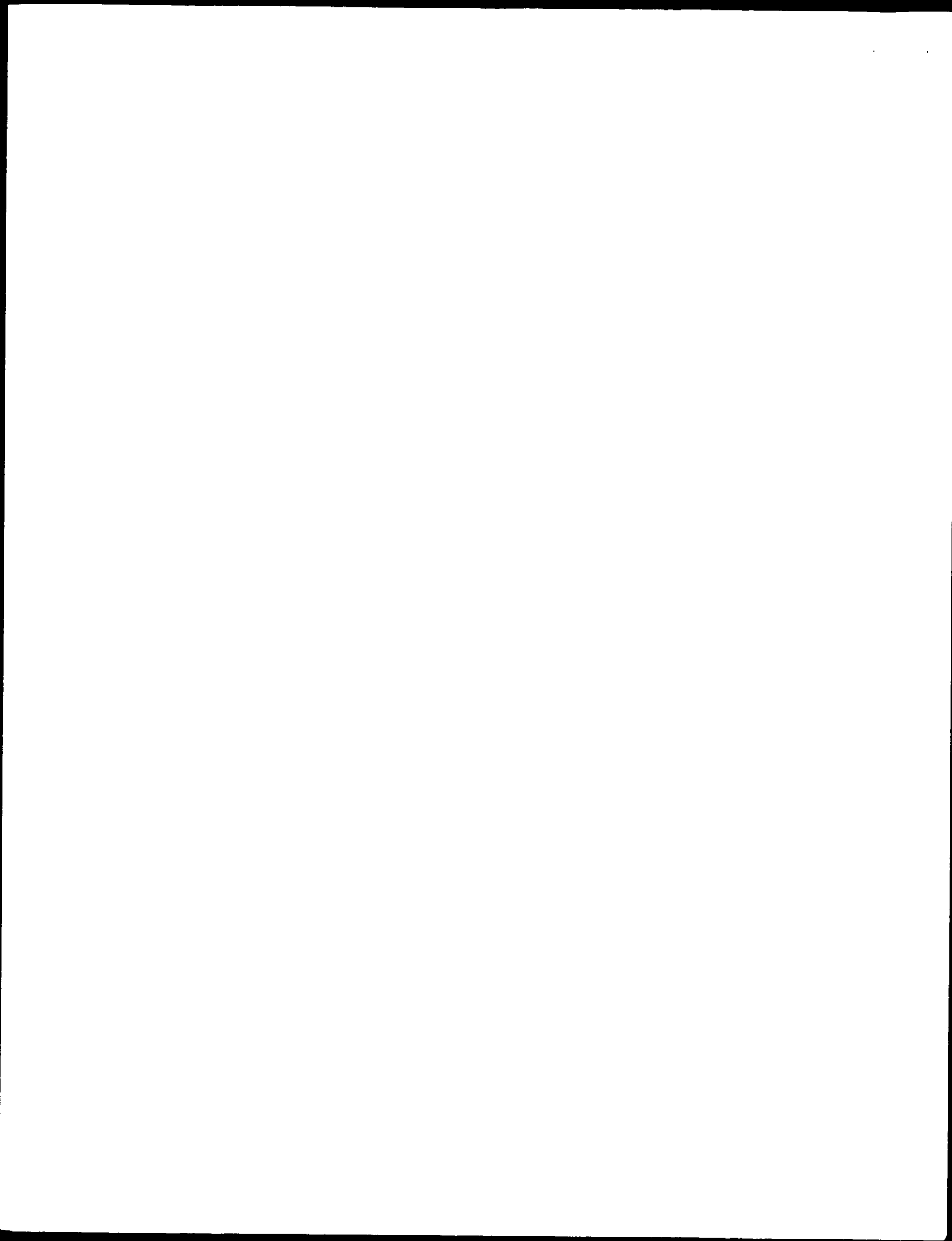
LA Japanese

=> s carotenoid? and plant(w)transform?

L6 18 CAROTENOID? AND PLANT(W) TRANSFORM?

=> duplicate remove l6

DUPLICATE PREFERENCE IS 'AGRICOLA, BIOSIS, EMBASE, CAPLUS'



KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L6

L7 9 DUPLICATE REMOVE L6 (9 DUPLICATES REMOVED)

=> d 17 1-9

L7 ANSWER 1 OF 9 CAPLUS COPYRIGHT 2003 ACS

AN 2002:123201 CAPLUS

DN 136:162385

TI Methyl-D-erythritol phosphate pathway gene gcpE from Arabidopsis thaliana and other plants

IN Boronat, Albert; Campos, Narciso; Rodriguez-Concepcion, Manuel; Rohmer, Michel; Seeman, Myriam; Valentin, Henry E.; Venkatesh, Tyamagondlu V.; Venkatramesh, Mylavaram

PA Monsanto Technology, LLC, USA

SO PCT Int. Appl., 155 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002012478	A2	20020214	WO 2001-US24335	20010806
	WO 2002012478	C1	20020704		
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
	AU 2001090522	A5	20020218	AU 2001-90522	20010806
	US 2002069426	A1	20020606	US 2001-921992	20010806
PRAI	US 2000-223483P	P	20000807		
	WO 2001-US24335	W	20010806		

L7 ANSWER 2 OF 9 CAPLUS COPYRIGHT 2003 ACS

AN 2002:963266 CAPLUS

TI Stimulation of ***carotenoid*** metabolism in arbuscular mycorrhizal roots

AU Fester, Thomas; Schmidt, Diana; Lohse, Swanhild; Walter, Michael H.; Giuliano, Giovanni; Bramley, Peter M.; Fraser, Paul D.; Hause, Bettina; Strack, Dieter

CS Leibniz-Institut für Pflanzenbiochemie, Abteilung Sekundärstoffwechsel, Halle/Saale, 06120, Germany

SO Planta (2002), 216(1), 148-154

CODEN: PLANAB; ISSN: 0032-0935

PB Springer-Verlag

DT Journal

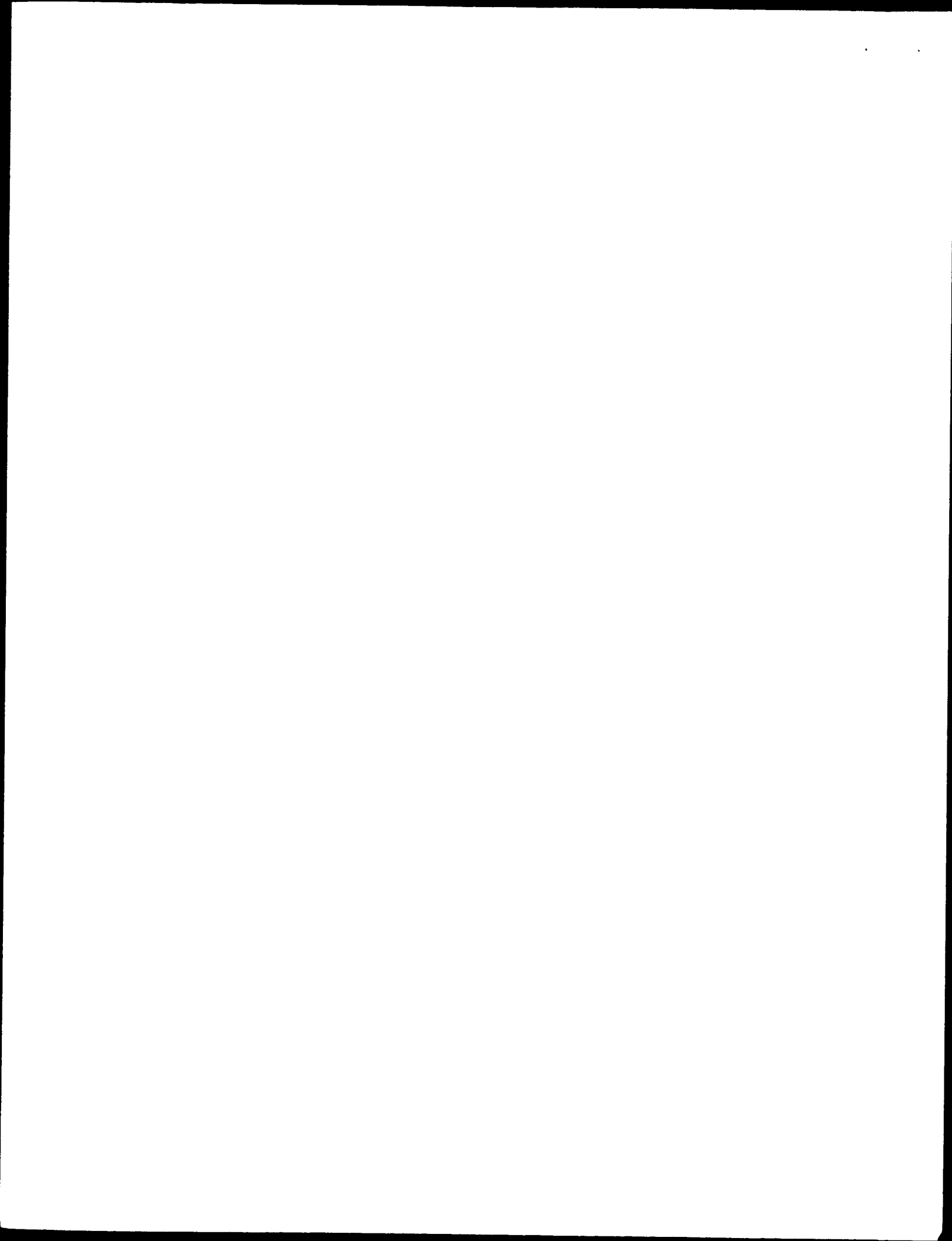
LA English

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1

AN 2001:37726 BIOSIS

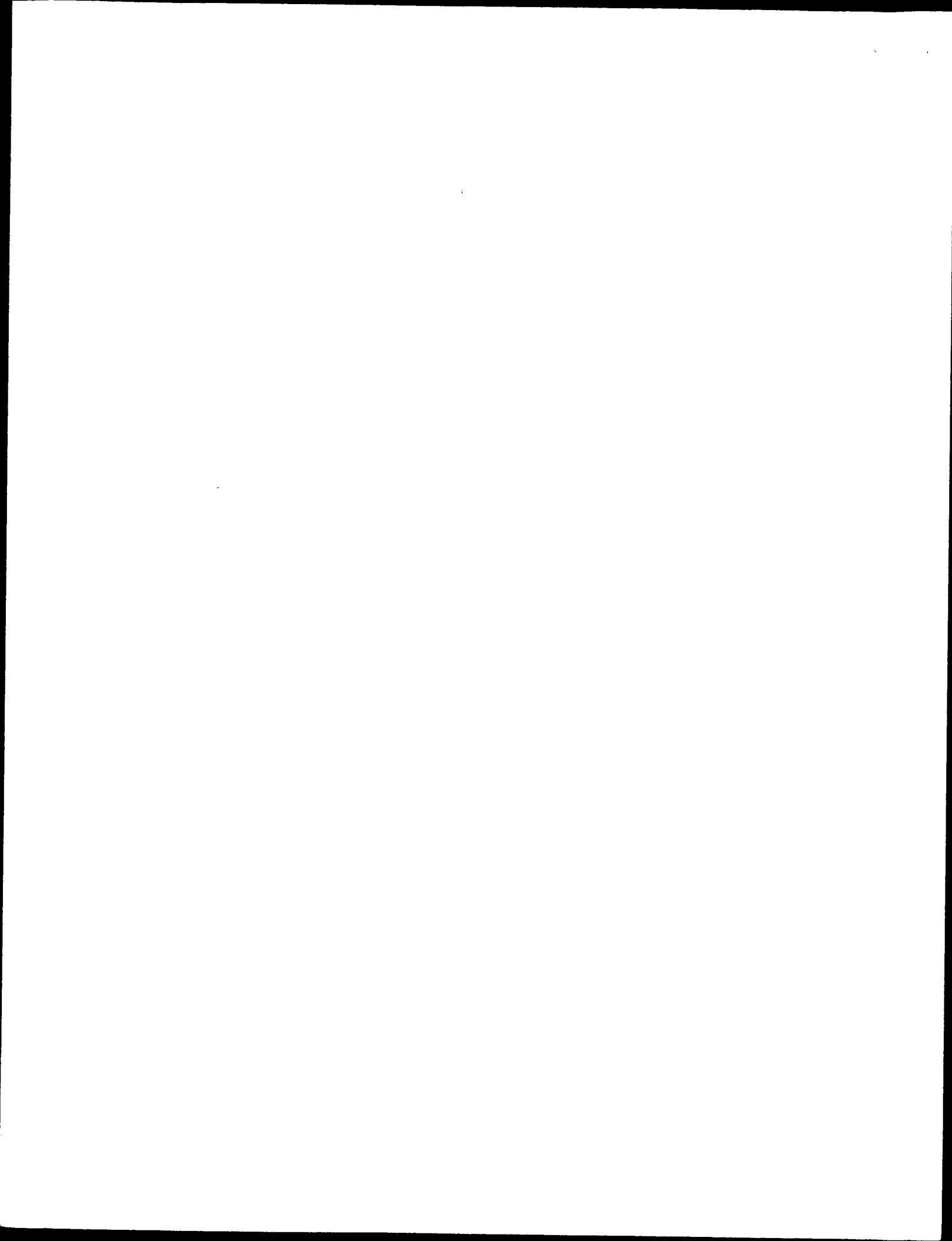


DN PREV200100037726
 TI The chloroplast and leaf developmental mutant, pale cress, exhibits light-conditional severity and symptoms characteristic of its ABA deficiency.
 AU Holding, David R. (1); Springer, Patricia S.; Coomber, Shirley A.
 CS (1) Department of Botany and Plant Sciences, University of California, Riverside, CA, 92521: dholding@ucr.edu USA
 SO Annals of Botany (London), (November, 2000) Vol. 86, No. 5, pp. 953-962. print.
 ISSN: 0305-7364.
 DT Article
 LA English
 SL English

L7 ANSWER 4 OF 9 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
 AN 2000311165 EMBASE
 TI Medicinal plant biotechnology: The Apiaceae family as the example of rapid development.
 AU Ekiert H.
 CS Dr. H. Ekiert, Dept. of Pharmaceutical Botany, Collegium Medicum, Jagiellonian University, 9 Medyczna Street, 30-688 Krakow, Poland. mfekiert@cyf-kr.edu.pl
 SO Pharmazie, (2000) 55/8 (561-567).
 Refs: 66
 ISSN: 0031-7144 CODEN: PHARAT
 CY Germany
 DT Journal; General Review
 FS 029 Clinical Biochemistry
 LA English
 SL English

L7 ANSWER 5 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2
 AN 2001:49727 BIOSIS
 DN PREV200100049727
 TI Identification of a novel gene coding for neoxanthin synthase from Solanum tuberosum.
 AU Al-Babili, Salim; Hugueney, Philippe; Schledz, Michael; Welsch, Ralf; Frohnmeier, Hanns; Laule, Oliver; Beyer, Peter (1)
 CS (1) Center for Applied Biosciences, University of Freiburg, Schaeenzlestr. 1, D-79104, Freiburg: beyer@uni-freiburg.de Germany
 SO FEBS Letters, (24 November, 2000) Vol. 485, No. 2-3, pp. 168-172. print.
 ISSN: 0014-5793.
 DT Article
 LA English
 SL English

L7 ANSWER 6 OF 9 CAPLUS COPYRIGHT 2003 ACS
 AN 1995:999495 CAPLUS
 DN 124:48378
 TI Studies on ***carotenoid*** biosynthesis using the methods of natural products chemistry, molecular biology, and metabolic engineering
 AU Misawa, Norihiko
 CS Cent. Lab. Key Technol., Kirin Brew. Co., Ltd., Yokohama, 236, Japan
 SO Nippon Nogei Kagaku Kaishi (1995), 69(12), 1567-72
 CODEN: NNKKA; ISSN: 0002-1407
 DT Journal; General Review
 LA Japanese



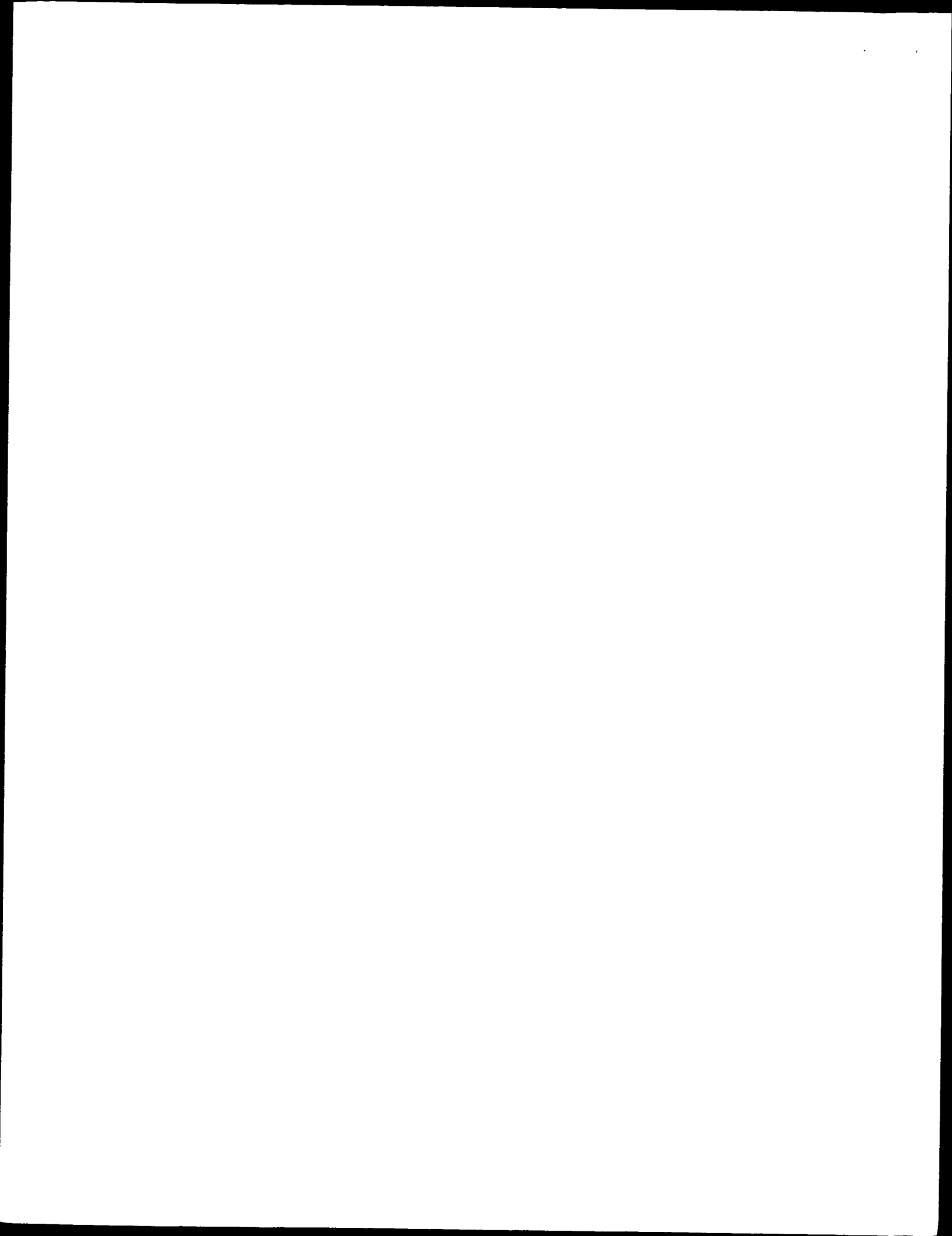
L7 ANSWER 7 OF 9 AGRICOLA DUPLICATE 3
 AN 97:60817 AGRICOLA
 DN IND20585833
 TI Constitutive expression of a fruit phytoene synthase gene in transgenic tomatoes causes dwarfism by redirecting metabolites from the gibberellin pathway.
 AU Fray, R.G.; Wallace, A.; Fraser, P.D.; Valero, D.; Hedden, P.; Bramley, P.M.; Grierson, D.
 CS Nottingham University, Loughborough, UK.
 SO The Plant journal : for cell and molecular biology, Nov 1995. Vol. 8, No. 5. p. 693-701
 Publisher: Oxford : Blackwell Scientific Publishers and BIOS Scientific Publishers in association with the Society for Experimental Biology, c1991-
 ISSN: 0960-7412
 NTE Includes references
 CY England; United Kingdom
 DT Article
 FS Non-U.S. Imprint other than FAO
 LA English

L7 ANSWER 8 OF 9 AGRICOLA DUPLICATE 4
 AN 94:73190 AGRICOLA
 DN IND20421086
 TI Engineering cyanobacterial models resistant to bleaching herbicides.
 AU Windhovel, U.; Geiges, B.; Sandmann, G.; Boger, P.
 AV DNAL (SB951.P49)
 SO Pesticide biochemistry and physiology, May 1994. Vol. 49, No. 1. p. 63-71
 Publisher: Orlando, Fla. : Academic Press.
 CODEN: PCBPBS; ISSN: 0048-3575
 NTE Includes references
 CY Florida; United States
 DT Article
 FS U.S. Imprints not USDA, Experiment or Extension
 LA English

L7 ANSWER 9 OF 9 AGRICOLA DUPLICATE 5
 AN 94:4347 AGRICOLA
 DN IND20363264
 TI Identification and genetic analysis of normal and mutant phytoene synthase genes of tomato by sequencing, complementation and co-suppression.
 AU Fray, R.G.; Grierson, D.
 AV DNAL (QK710.P62)
 SO Plant molecular biology, July 1993. Vol. 22, No. 4. p. 589-602
 Publisher: Dordrecht : Kluwer Academic Publishers.
 CODEN: PMBIDB; ISSN: 0167-4412
 NTE Includes references
 CY Netherlands
 DT Article
 FS Non-U.S. Imprint other than FAO
 LA English

=> FIL STNGUIDE
 COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION



FULL ESTIMATED COST

32.89

55.29

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FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Feb 14, 2003 (20030214/UP).

=> d l7 7 ab ibib
YOU HAVE REQUESTED DATA FROM FILE 'AGRICOLA, BIOSIS, EMBASE, CAPLUS' - CONTINUE?
(Y)/N:y

L7 ANSWER 7 OF 9 AGRICOLA DUPLICATE 3
AB Tomato ***plants*** ***transformed*** with a copy of the
fruit-expressed phytoene synthase cDNA under control of the CaMV 35S
promoter showed ectopic production of ***carotenoids***. High
expressers were reduced in stature. The dwarf character was inherited with
an inverse relationship between expression of phytoene synthase and plant
height. Severely affected plants also showed reduced chlorophyll content
in young leaves. These dwarfs showed a 30-fold reduction in levels of
gibberellin A1 (GA1) and growth was partially restored by treatment with
exogenous GA3. Qualitative and quantitative changes in ***carotenoids***
were also found. It is proposed that the dwarf phenotype results from the
over-production of phytoene synthase, which converts geranylgeranyl
diphosphate to phytoene and thereby diverts this intermediate away from
the gibberellin (GA) and phytol biosynthetic pathways.
ACCESSION NUMBER: 97:60817 AGRICOLA
DOCUMENT NUMBER: IND20585833
TITLE: Constitutive expression of a fruit phytoene synthase
gene in transgenic tomatoes causes dwarfism by
redirecting metabolites from the gibberellin pathway.
AUTHOR(S): Fray, R.G.; Wallace, A.; Fraser, P.D.; Valero, D.;
Hedden, P.; Bramley, P.M.; Grierson, D.
CORPORATE SOURCE: Nottingham University, Loughborough, UK.
SOURCE: The Plant journal : for cell and molecular biology,
Nov 1995. Vol. 8, No. 5. p. 693-701
Publisher: Oxford : Blackwell Scientific Publishers
and BIOS Scientific Publishers in association with the
Society for Experimental Biology, c1991-
ISSN: 0960-7412
NOTE: Includes references
PUB. COUNTRY: England; United Kingdom
DOCUMENT TYPE: Article
FILE SEGMENT: Non-U.S. Imprint other than FAO
LANGUAGE: English

=> s terminal(w)oxidase and carotenoid and plant
11 TERMINAL
0 OXIDASE
0 TERMINAL(W)OXIDASE
0 CAROTENOID
13 PLANT

6 PLANTS
19 PLANT
(PLANT OR PLANTS)
L8 0 TERMINAL(W)OXIDASE AND CAROTENOID AND PLANT

=> file agricola biosis embase caplus
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.36	59.77

FULL ESTIMATED COST

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FILE 'BIOSIS' ENTERED AT 18:33:18 ON 20 FEB 2003
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=> s terminal(w)oxidase and carotenoid and plant
L9 19 TERMINAL(W) OXIDASE AND CAROTENOID AND PLANT

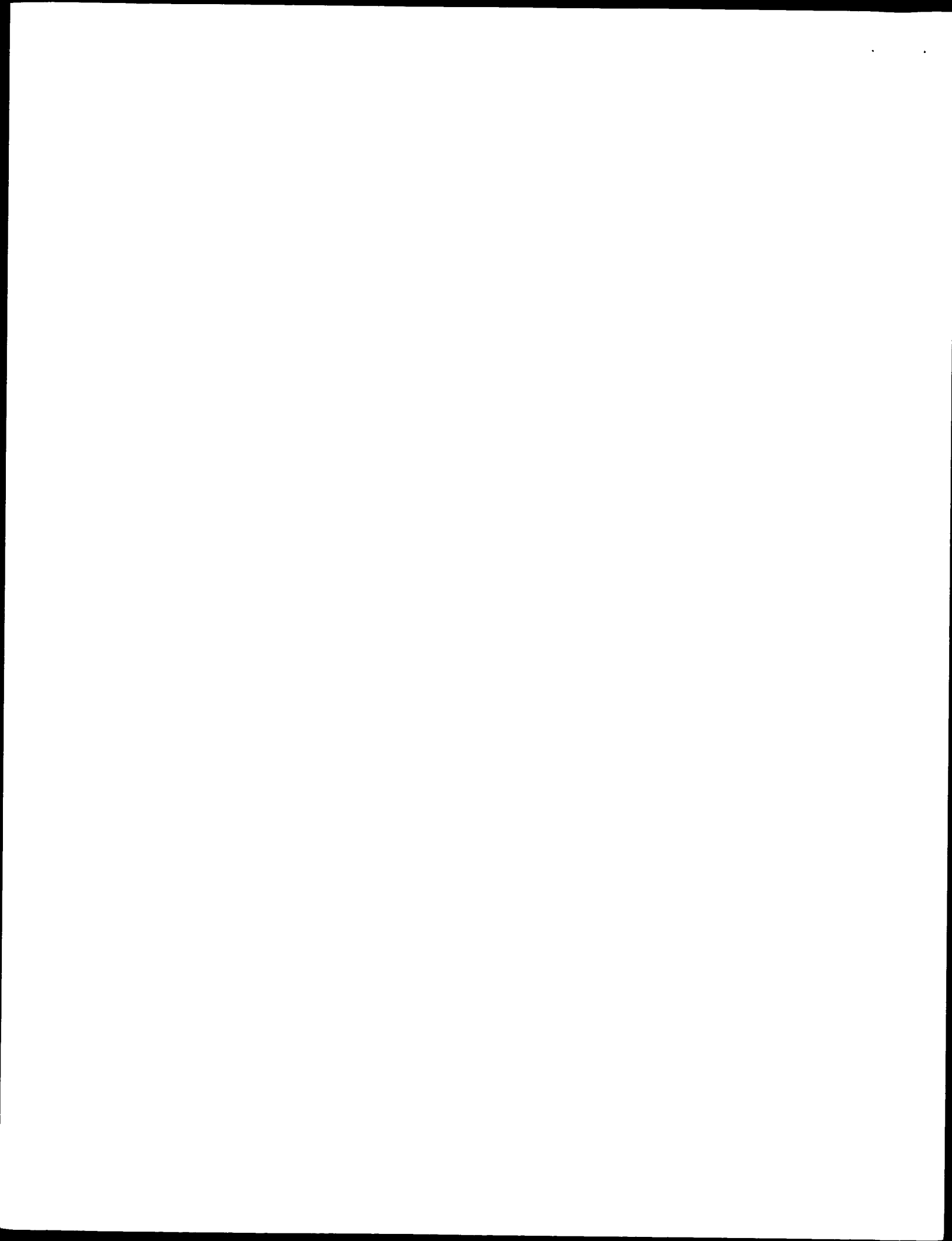
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DUPLICATE PREFERENCE IS 'AGRICOLA, BIOSIS, EMBASE, CAPLUS'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n
PROCESSING COMPLETED FOR L9
L10 10 DUPLICATE REMOVE L9 (9 DUPLICATES REMOVED)

=> d l10 1-10

L10 ANSWER 1 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE
1
AN 2002:526871 BIOSIS
DN PREV200200526871
TI Involvement of a plastid ***terminal*** ***oxidase*** in
plastoquinone oxidation as evidenced by expression of the Arabidopsis
thaliana enzyme in tobacco.
AU Joet, Thierry; Genty, Bernard; Josse, Eve-Marie; Kuntz, Marcel; Cournac,
Laurent; Peltier, Gilles (1)
CS (1) Direction des Sciences du Vivant, Departement d'Ecophysiologie
Vegetale et de Microbiologie, Laboratoire d'Ecophysiologie de la
Photosynthese, CEA Cadarache, Unite Mixte de Recherche 163 CNRS CEA,
Univ-Mediterranee, CEA1000, 13108, Saint-Paul-lez-Durance Cedex:
gilles.peltier@cea.fr France
SO Journal of Biological Chemistry, (August 30, 2002) Vol. 277, No. 35, pp.
31623-31630. <http://www.jbc.org/>. print.
ISSN: 0021-9258.
DT Article
LA English

L10 ANSWER 2 OF 10 AGRICOLA
AN 2001:23319 AGRICOLA
DN IND22300531

DUPLICATE 2



TI A plastid ***terminal*** ***oxidase*** comes to light:
 implications for ***carotenoid*** biosynthesis and chlororespiration.
 AU Carol, P.; Kuntz, M.
 AV DNAL (QK1.T74)
 SO Trends in plant science, Jan 2001. Vol. 6, No. 1. p. 31-36
 Publisher: Kidlington, Oxford : Elsevier Science, Ltd., c1996-
 ISSN: 1360-1385
 NTE Includes references
 CY England; United Kingdom
 DT Article; Law
 FS Non-U.S. Imprint other than FAO
 LA English

L10 ANSWER 3 OF 10 CAPLUS COPYRIGHT 2003 ACS

AN 2000:278123 CAPLUS

DN 132:318612

TI Arabidopsis ***terminal*** ***oxidase*** associated with
 carotenoid biosynthesis, modification of ***plant***
 carotenoid biosynthesis, and method for herbicide screening

IN Carol, Pierre; Kuntz, Marcel; Mache, Regis

PA Universite Joseph Fourier, Fr.

SO PCT Int. Appl., 53 pp.

CODEN: PIXXD2

DT Patent

LA French

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000023605	A1	20000427	WO 1999-IB1719	19991020
	W: CA, IL, JP, US				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	FR 2784688	A1	20000421	FR 1998-13283	19981020
	FR 2784688	B1	20021213		
	EP 1123406	A1	20010816	EP 1999-952734	19991020
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 2002527113	T2	20020827	JP 2000-577312	19991020
PRAI	FR 1998-13283	A	19981020		
	WO 1999-IB1719	W	19991020		

RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 4 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

AN 2001:56235 BIOSIS

DN PREV200100056235

TI In vitro and in situ inhibition of ***carotenoid*** biosynthesis in
 Capsicum annuum by bleaching herbicides.

AU Simkin, Andrew J.; Breitenbach, Jurgen; Kuntz, Marcel (1); Sandmann,
 Gerhard

CS (1) Genetique Moleculaire des Plantes, CNRS (UMR5575), Universite J.
 Fourier, F-38041, Grenoble Cedex, 9: marcel.kuntz@ujf-grenoble.fr France

SO Journal of Agricultural and Food Chemistry, (October, 2000) Vol. 48, No.
 10, pp. 4676-4680. print.

ISSN: 0021-8561.

DT Article

LA English

SL English

L10 ANSWER 5 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE
3

AN 2000:452024 BIOSIS

DN PREV200000452024

TI A plastid ***terminal*** ***oxidase*** associated with
carotenoid desaturation during chromoplast differentiation.

AU Josse, Eve-Marie; Simkin, Andrew J.; Gaffe, Joel; Laboure, Anne-Marie;
Kuntz, Marcel (1); Carol, Pierre

CS (1) Laboratoire de Genetique Moleculaire des Plantes, Unite Mixte de
Recherche 5575, Universite Joseph Fourier, Centre National de la Recherche
Scientifique, 38041, Grenoble Cedex 9 France

SO Plant Physiology (Rockville), (August, 2000) Vol. 123, No. 4, pp.
1427-1436. print.

ISSN: 0032-0889.

DT Article

LA English

SL English

L10 ANSWER 6 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

AN 2000:533098 BIOSIS

DN PREV200000533098

TI A plastid ***terminal*** ***oxidase*** associated with
carotenoid desaturation during chromoplast differentiation.

AU Josse, E.-M. (1); Simkin, A. J. (1); Gaffe, J. (1); Laboure, A.-M. (1);
Kuntz, M. (1); Carol, P. (1)

CS (1) Laboratoire de Genetique Moleculaire des Plantes, Universite Joseph
Fourier and CNRS (UMR 5575), 38041, Grenoble Cedex 9 France

SO Plant Physiology and Biochemistry (Paris), (August, 2000) Vol. 38, No.
Supplement, pp. s265. print.

Meeting Info.: 12th Congress of the Federation of European Societies of
Plant Physiology Budapest, Hungary August 21-25, 2000

ISSN: 0981-9428.

DT Conference

LA English

SL English

L10 ANSWER 7 OF 10 AGRICOLA

DUPLICATE 4

AN 1999:59000 AGRICOLA

DN IND21996880

TI Mutations in the Arabidopsis gene IMMUTANS cause a variegated phenotype by
inactivating a chloroplast ***terminal*** ***oxidase*** associated
with phytoene desaturation.

AU Carol, P.; Stevenson, D.; Bisanz, C.; Breitenbach, J.; Sandmann, G.;
Mache, R.; Coupland, G.; Kuntz, M.

CS Universite Joseph Fourier, Grenoble, France.

AV DNAL (QK725.P532)

SO The Plant cell, Jan 1999. Vol. 11, No. 1. p. 57-68

Publisher: [Rockville, MD : American Society of Plant Physiologists,
c1989-

CODEN: PLCEEW; ISSN: 1040-4651

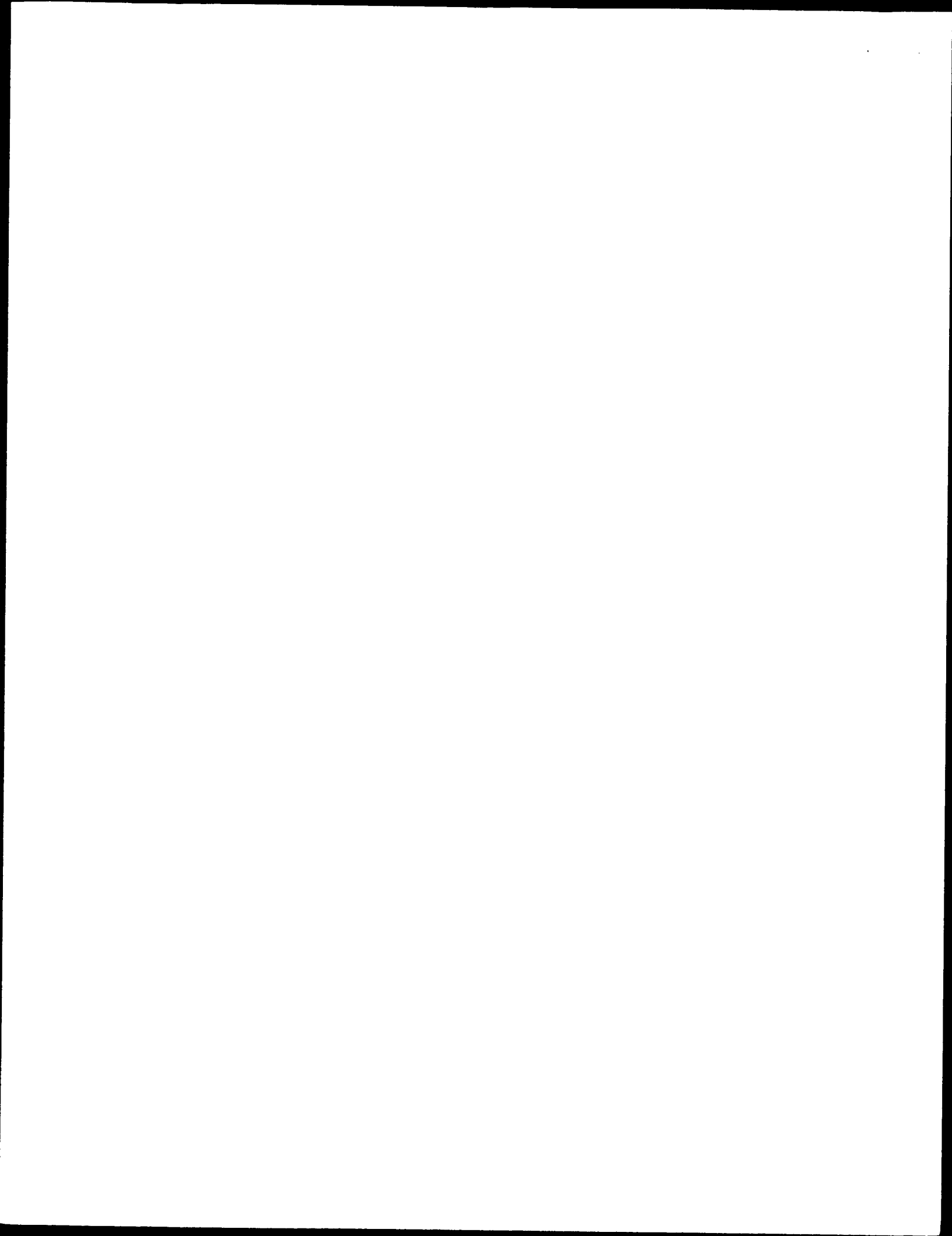
NTE Includes references

CY Maryland; United States

DT Article

FS U.S. Imprints not USDA, Experiment or Extension

LA English



L10 ANSWER 8 OF 10 AGRICOLA DUPLICATE 5
 AN 1999:58999 AGRICOLA
 DN IND21996873
 TI The IMMUTANS variegation locus of Arabidopsis defines a mitochondrial alternative oxidase homology that functions during early chloroplast biogenesis.
 AU Wu, D.; Wright, D.A.; Wetzels, C.; Voytas, D.F.; Rodermel, D.
 CS Iowa State University, Ames, IA.
 AV DNAL (QK725.P532)
 SO The Plant cell, Jan 1999. Vol. 11, No. 1. p. 43-55
 Publisher: [Rockville, MD : American Society of Plant Physiologists, c1989-
 CODEN: PLCEEW; ISSN: 1040-4651
 NTE Includes references
 CY Maryland; United States
 DT Article
 FS U.S. Imprints not USDA, Experiment or Extension
 LA English

L10 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2003 ACS
 AN 1963:476714 CAPLUS
 DN 59:76714
 OREF 59:14302a-d
 TI Dependence of oxygen absorption by green and nongreen leaves on the intensity and spectral composition of light
 AU Voskresenskaya, N. P.
 SO Fiziol. Drevesn. Rastenii (or:Moscow: Akad. Nauk SSSR (1962) 150-9
 From: Ref. Zh., Biol. Khim. 1963, Abstr. No. 11F704.
 DT Journal
 LA Unavailable

L10 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2003 ACS
 AN 1961:138228 CAPLUS
 DN 55:138228
 OREF 55:26143h-i,26144a
 TI Effect of shortwave radiation on absorption of oxygen by ***plant*** leaves
 AU Voskresenskaya, N. P.
 CS K. A. Timiryazev Inst. Plant Physiol., Moscow
 SO Problemy Fotosinteza, Doklady 2-oi [Vtoroi] Konf., Moscow (1959), Volume Date 1957 335-45
 DT Journal
 LA Unavailable

=> FIL STNGUIDE

COST IN U.S. DOLLARS

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ENTRY

SESSION

FULL ESTIMATED COST

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82.19

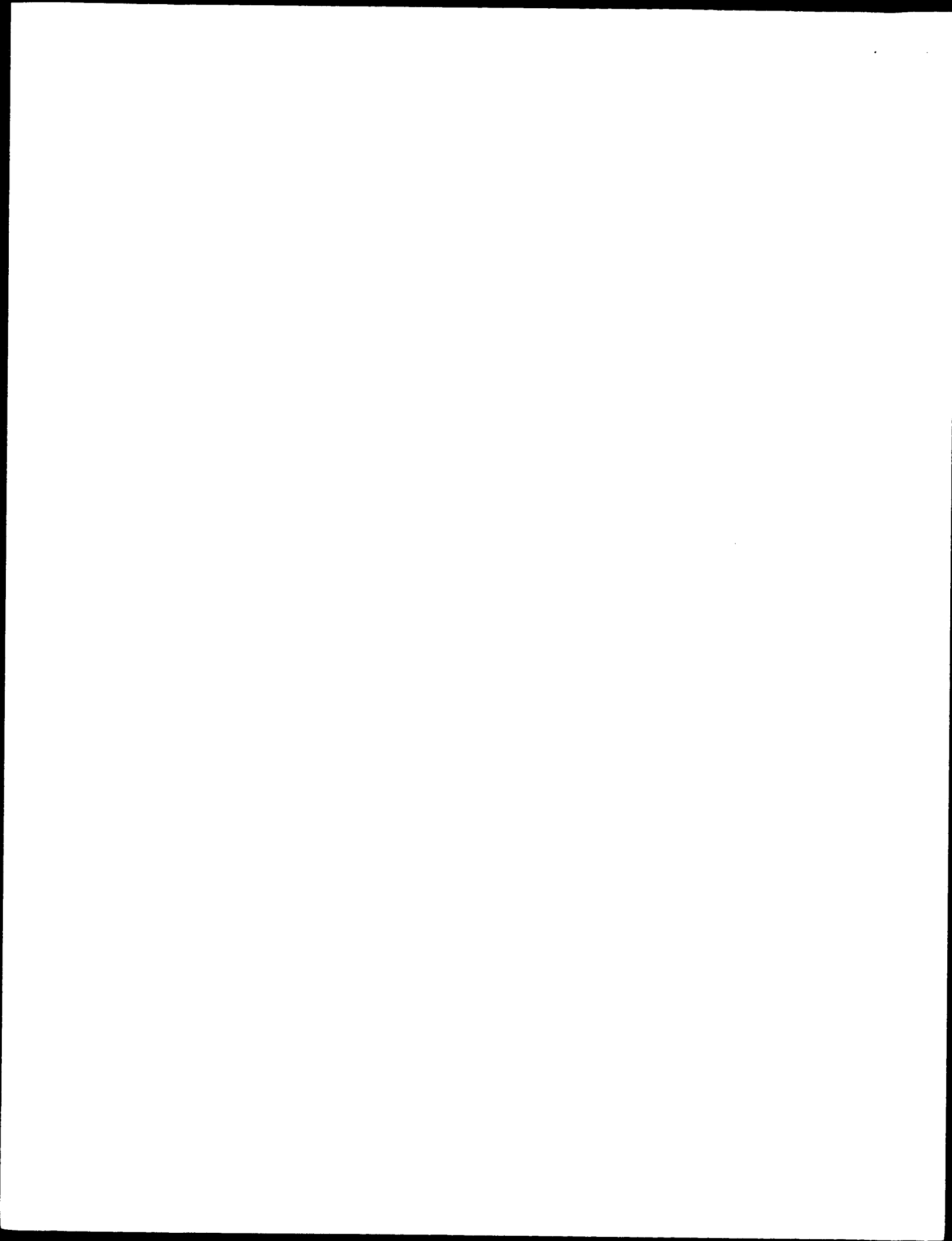
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LAST RELOADED: Feb 14, 2003 (20030214/UP).

=> s carotenoid and transform?

0 CAROTENOID

0 TRANSFORM?

L11 0 CAROTENOID AND TRANSFORM?

=> file agricola biosis embase caplus

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

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82.55

FILE 'AGRICOLA' ENTERED AT 18:39:33 ON 20 FEB 2003

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=> s carotenoid and transform?

L12 1307 CAROTENOID AND TRANSFORM?

=> s l12 and plant

L13 370 L12 AND PLANT

=> duplicate remove l13

DUPLICATE PREFERENCE IS 'AGRICOLA, BIOSIS, EMBASE, CAPLUS'

KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L13

L14 287 DUPLICATE REMOVE L13 (83 DUPLICATES REMOVED)

=> s l14 and transgenic

L15 61 L14 AND TRANSGENIC

=> d l15 51-61

L15 ANSWER 51 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1996:637967 CAPLUS

DN 125:294058

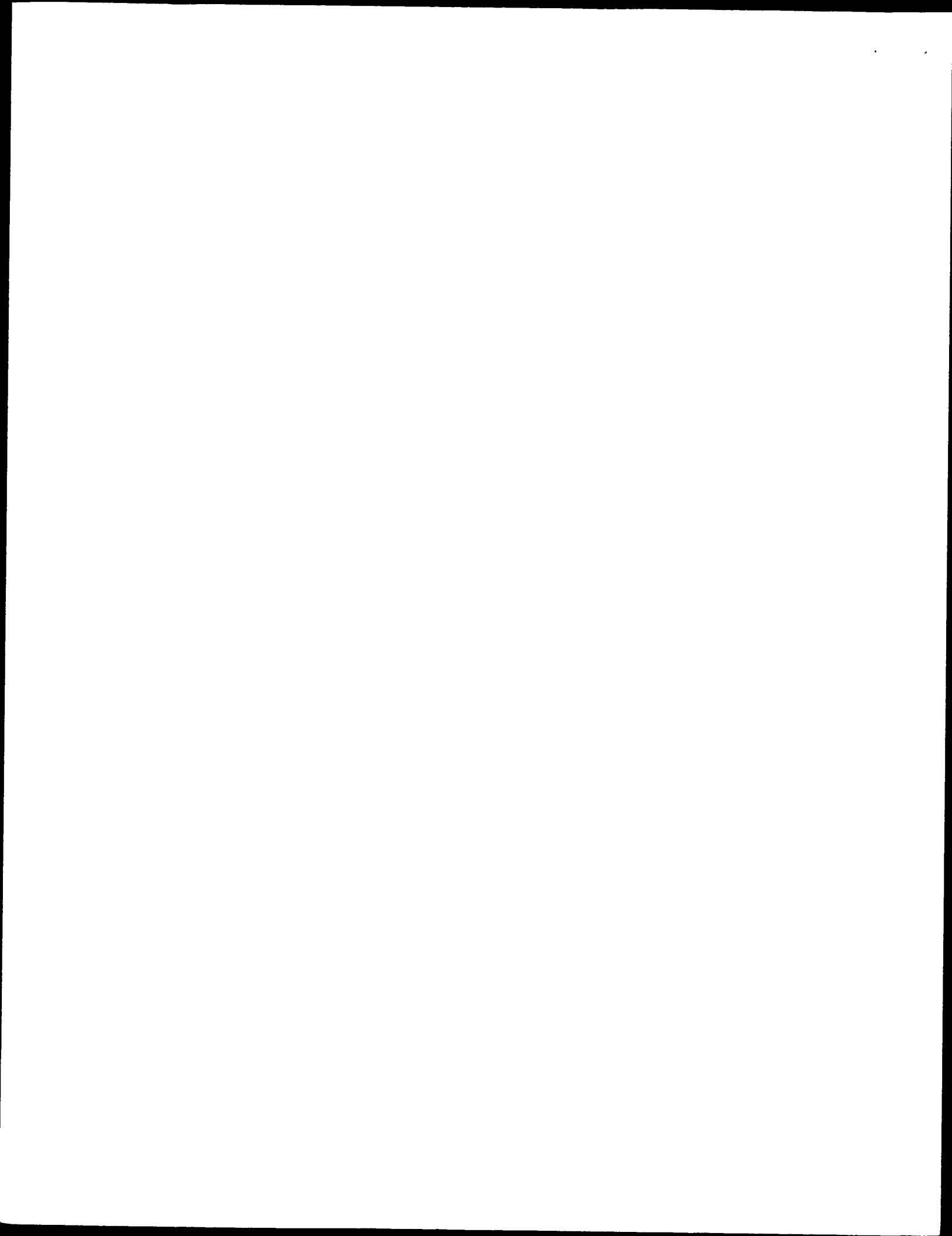
TI Use of gene silencing to probe ***carotenoid*** gene expression in
tomato

AU Fray, R. G.; Hamilton, A. J.; Grierson, D.; Davey, M. R.; Blackhall, N. W.
CS Dep. of Physiology and Environmental Science, Univ. of Nottingham, Leics,
UK

SO Mechanisms and Applications of Gene Silencing, [Easter School in
Agricultural Science], 57th, Sutton Bonington, UK, Mar., 1995 (1996),
Meeting Date 1995, 49-55, 8 plates. Editor(s): Grierson, Donald; Lycett,
Grantley W.; Tucker, Gregory A. Publisher: Nottingham University Press,
Nottingham, UK.

CODEN: 63NBAT

DT Conference; General Review



LA English

L15 ANSWER 52 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1996:481698 CAPLUS

DN 125:137740

TI Manipulating ***carotenoids*** in ***transgenic*** ***plants***

AU Schuch, Wolfgang; Drake, Rachel; Romer, Susanne; Bramley, Peter M.

CS Zeneca Plant Science, Jealott's Hill Research Station,
Bracknell/Berkshire, RG42 6EY, UK

SO Annals of the New York Academy of Sciences (1996), 792 (Engineering Plants
for Commercial Products and Applications), 13-19

CODEN: ANYAA9; ISSN: 0077-8923

PB New York Academy of Sciences

DT Journal; General Review

LA English

L15 ANSWER 53 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1996:410595 CAPLUS

DN 125:82197

TI Increasing yields of ***carotenoids*** in ***plants*** by
expression of genes for microbial phytoene synthases in storage organs

IN Hauptmann, Randal; Eschenfeldt, William H.; English, Jami; Brinkhaus,
Friedhelm L.

PA Amoco Corporation, USA

SO PCT Int. Appl., 105 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	WO 9613149	A1	19960509	WO 1995-US13937	19951027
	W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, JP, KE, KG,				
	KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL,				
	RO, RU, SD, SI, SK, TJ, TT, UA, UZ, VN				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	CA 2203815	AA	19960509	CA 1995-2203815	19951027
	AU 9539701	A1	19960523	AU 1995-39701	19951027
	AU 697358	B2	19981001		
	EP 792352	A1	19970903	EP 1995-937660	19951027
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	CN 1172416	A	19980204	CN 1995-197153	19951027
	PL 182161	B1	20011130	PL 1995-319788	19951027
PRAI	US 1994-331004	A	19941028		
	WO 1995-US13937	W	19951027		

L15 ANSWER 54 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1995:1004323 CAPLUS

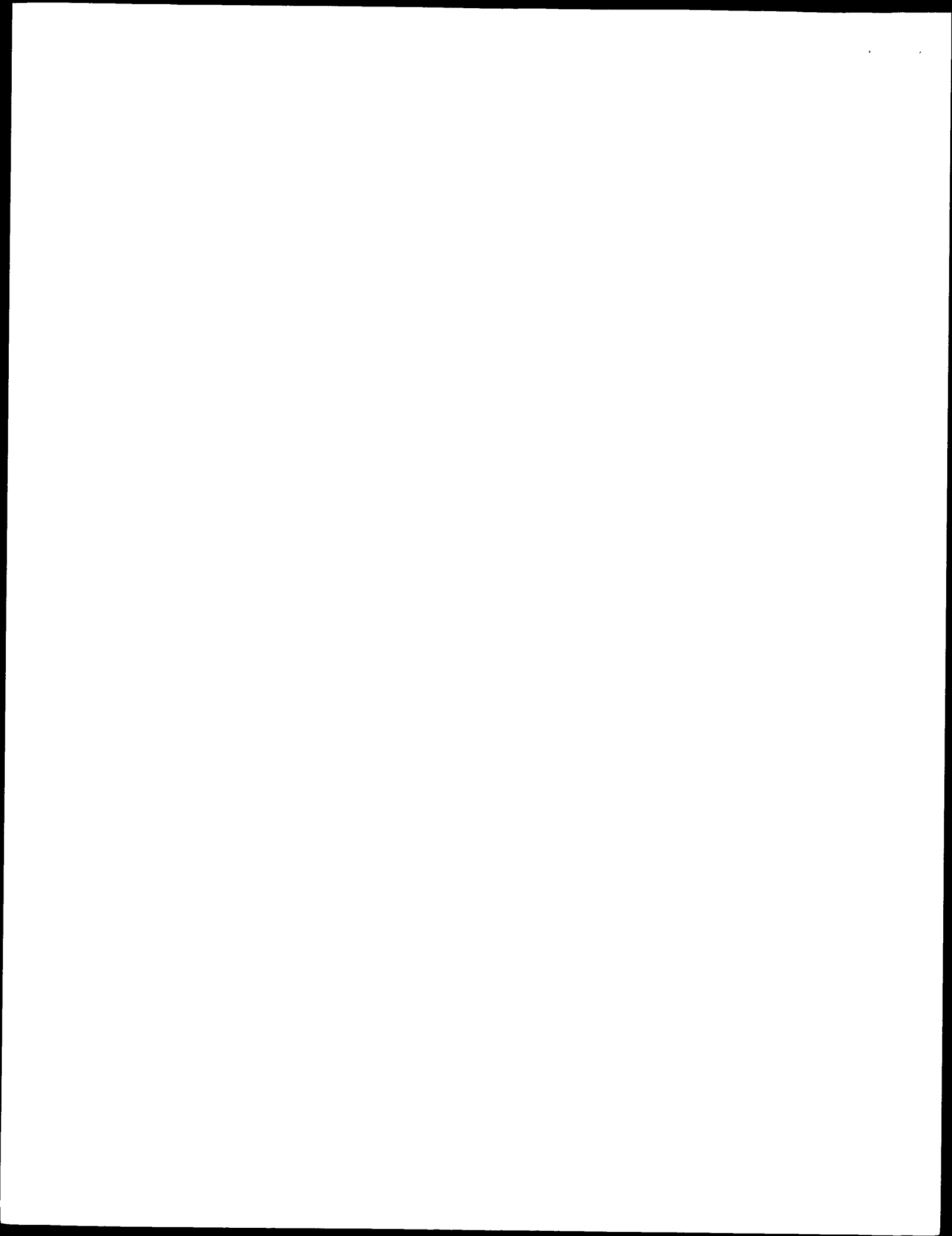
DN 124:50735

TI Is the reaction catalyzed by 3-hydroxy-3-methylglutaryl coenzyme A
reductase a rate-limiting step for isoprenoid biosynthesis in
plants ?

AU Chappell, Joseph; Wolf, Fred; Proulx, Jeanne; Cuellar, Rick; Saunders,
Court

CS Plant Physiology/Biochemistry/Molecular Biology Program, University of
Kentucky, Lexington, KY, 40546-0091, USA

SO Plant Physiology (1995), 109(4), 1337-43



CODEN: PLPHAY; ISSN: 0032-0889

PB American Society of Plant Physiologists
DT Journal
LA English

L15 ANSWER 55 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1995:742328 CAPLUS

DN 123:139151

TI Violaxanthin cycle pigment contents in potato and tobacco ***plants***
with genetically reduced photosynthetic capacity

AU Bilger, Wolfgang; Fisahn, Joachim; Brummet, Wolfgang; Kossmann, Jens;
Willmitzer, Lothar

CS Julius-von-Sachs-Inst. Biowissenschaften, Lehrstuhl Botanik II, Wuerzburg,
97082, Germany

SO Plant Physiology (1995), 108(4), 1479-86

CODEN: PLPHAY; ISSN: 0032-0889

PB Dekker

DT Journal

LA English

L15 ANSWER 56 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1994:428078 CAPLUS

DN 121:28078

TI Functional expression of the Erwinia uredovora ***carotenoid***
biosynthesis gene crtI in ***transgenic*** ***plants*** showing an
increase of .beta.-carotene biosynthesis activity and resistance to the
bleaching herbicide norflurazon. [Erratum to document cited in
CA120(17):209642b]

AU Misawa, Norihiko; Yamano, Shigeyuki; Linden, Hartmut; de Felipe, Maria R.;
Lucas, Mercedes; Ikenaga, Hiroshi; Sandmann, Gerhard

CS Cent. Lab. Key Technol., Kirin Brew. Co., Ltd., Yokohma, 236, Japan

SO Plant Journal (1994), 5(2), 309

CODEN: PLJUED; ISSN: 0960-7412

DT Journal

LA English

L15 ANSWER 57 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1994:209642 CAPLUS

DN 120:209642

TI Functional expression of the Erwinia uredovora ***carotenoid***
biosynthesis gene crtI in ***transgenic*** ***plants*** showing an
increase of .beta.-carotene biosynthesis activity and resistance to the
bleaching herbicide norflurazon

AU Misawa, Norihiko; Yamano, Shigeyuki; Linden, Hartmut; de Felipe, Maria R.;
Lucas, Mercedes; Ikenaga, Hiroshi; Sandmann, Gerhard

CS Cent. Lab. Key Technol., Kirin Brew. Co., Ltd, Yokohama, 236, Japan

SO Plant Journal (1993), 4(5), 833-40

CODEN: PLJUED; ISSN: 0960-7412

DT Journal

LA English

L15 ANSWER 58 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1994:158389 CAPLUS

DN 120:158389

TI Study on the ***carotenoid*** biosynthetic pathway at the level of the
genes and enzymes

AU Misawa, N.; Yamano, S.; Kobayashi, K.; Ikenaga, H.; Nakagawa, M.;

Harashima, K.; Sandmann, G.; Linden, H.
 CS Cent. Lab., Key Tech. Kirin Brewery Co., Ltd., Japan
 SO Tennen Yuki Kagobutsu Toronkai Koen Yoshishu (1992), 34th, 212-219
 CODEN: TYKYDS
 DT Journal
 LA Japanese

L15 ANSWER 59 OF 61 CAPLUS COPYRIGHT 2003 ACS
 AN 1992:35644 CAPLUS
 DN 116:35644
 TI Biosynthesis of ***carotenoids*** in genetically engineered hosts
 IN Ausich, Rodney Lee; Brinkhaus, Friedhelm Luetke; Mukharji, Indrani;
 Proffitt, John Houston; Yarger, James Gregory; Yen, Huei Che Bill
 PA Amoco Corp., USA
 SO PCT Int. Appl., 311 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9113078	A1	19910905	WO 1991-US1458	19910304
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	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE				
	EP 471056	A1	19920219	EP 1991-905713	19910304
	EP 471056	B1	20011017		
	R: BE, CH, DE, DK, FR, GB, IT, LI, NL				
	JP 05504686	T2	19930722	JP 1991-506139	19910304
	US 5545816	A	19960813	US 1993-93577	19930719
	US 5530188	A	19960625	US 1993-95726	19930721
	US 5530189	A	19960625	US 1993-96043	19930722
	US 5684238	A	19971104	US 1993-96623	19930722
	US 5656472	A	19970812	US 1995-473512	19950607
PRAI	US 1990-487613	A	19900302		
	US 1990-525551	A	19900518		
	US 1990-562674	A	19900803		
	US 1991-662921	A	19910228		
	WO 1991-US1458	U	19910304		
	US 1991-785566	B1	19911030		
	US 1991-785568	B1	19911030		
	US 1991-785569	B1	19911030		
	US 1991-805061	B1	19911209		
	US 1993-95726	A3	19930721		

L15 ANSWER 60 OF 61 CAPLUS COPYRIGHT 2003 ACS
 AN 1991:649578 CAPLUS
 DN 115:249578
 TI Effects of sense and antisense transcripts of lycopene biosynthesis gene
 on fruit and flower color
 IN Bird, Colin Roger; Grierson, Donald; Schuch, Wolfgang Walter
 PA Imperial Chemical Industries PLC, UK
 SO PCT Int. Appl., 31 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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    AU 9168938      A1  19910718      AU 1991-68938        19901210
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    EP 505405       A1  19920930      EP 1991-900277      19901210
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    JP 05502160     T2  19930422      JP 1991-500993      19901210
    EP 699765       A1  19960306      EP 1995-111177      19901210
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    US 5304478      A   19940419      US 1992-995950      19921228
    US 5750865      A   19980512      US 1994-300582      19940902
PRAI GB 1989-28179      19891213
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    WO 1990-GB1924      19901210
    US 1990-625664      19901213
    US 1992-859523      19920812

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L15  ANSWER 61 OF 61  CAPLUS  COPYRIGHT 2003 ACS
AN   1988:164906  CAPLUS
DN   108:164906
TI   A DNA-liposome transfection product in pea with pigment changes
AU   Ahokas, Hannu
CS   Dep. Genet., Univ. Helsinki, Helsinki, SF-00100, Finland
SO   Annales Botanici Fennici (1987), 24(3), 245-50
      CODEN: ABOFAQ; ISSN: 0003-3847
DT   Journal
LA   English

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FULL ESTIMATED COST                21.10      103.65

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USE IS SUBJECT TO THE TERMS OF YOUR CUSTOMER AGREEMENT
COPYRIGHT (C) 2003 AMERICAN CHEMICAL SOCIETY, JAPAN SCIENCE
AND TECHNOLOGY CORPORATION, AND FACHINFORMATIONSZENTRUM KARLSRUHE

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FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Feb 14, 2003 (20030214/UP).

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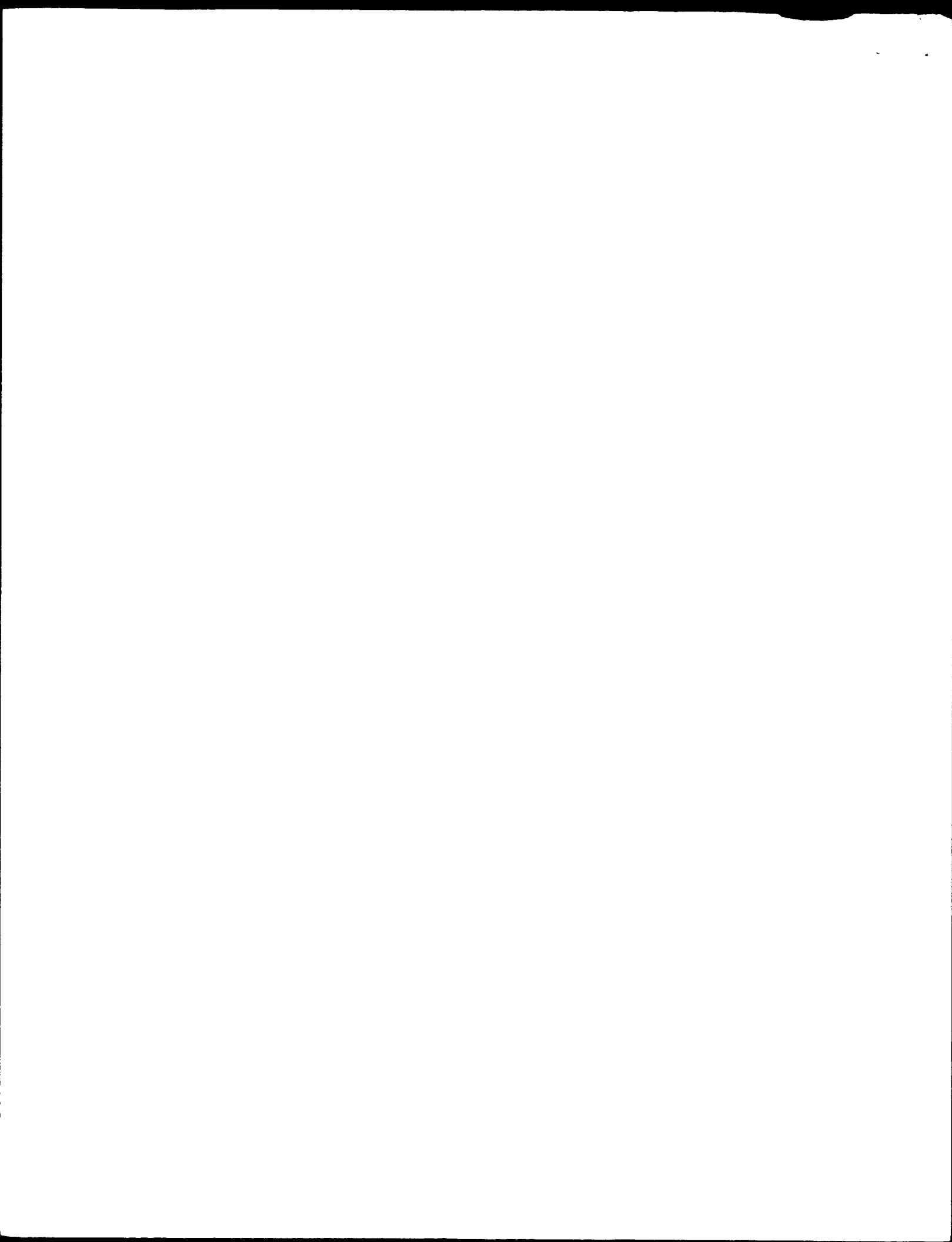
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JOURNAL
REFERENCE
AUTHORS
TITLE

Submitted (18-MAR-1998) Carol P., Genetique Moleculaire des
Plantes, Université Joseph Fourier, Cermo, 460 rue de la Piscine,
Saint Martin d'heres, 38053, FRANCE
2 (bases 1 to 1396)
Carol P., Stevenson, D., Kuntz, M., Coupland, G. and Wache, R.
The mutants locus of arabidopsis encodes a chloroplast alternative
oxidase-like protein involved in phytoene desaturation

CHARACTERISTICS	Location/Qualification
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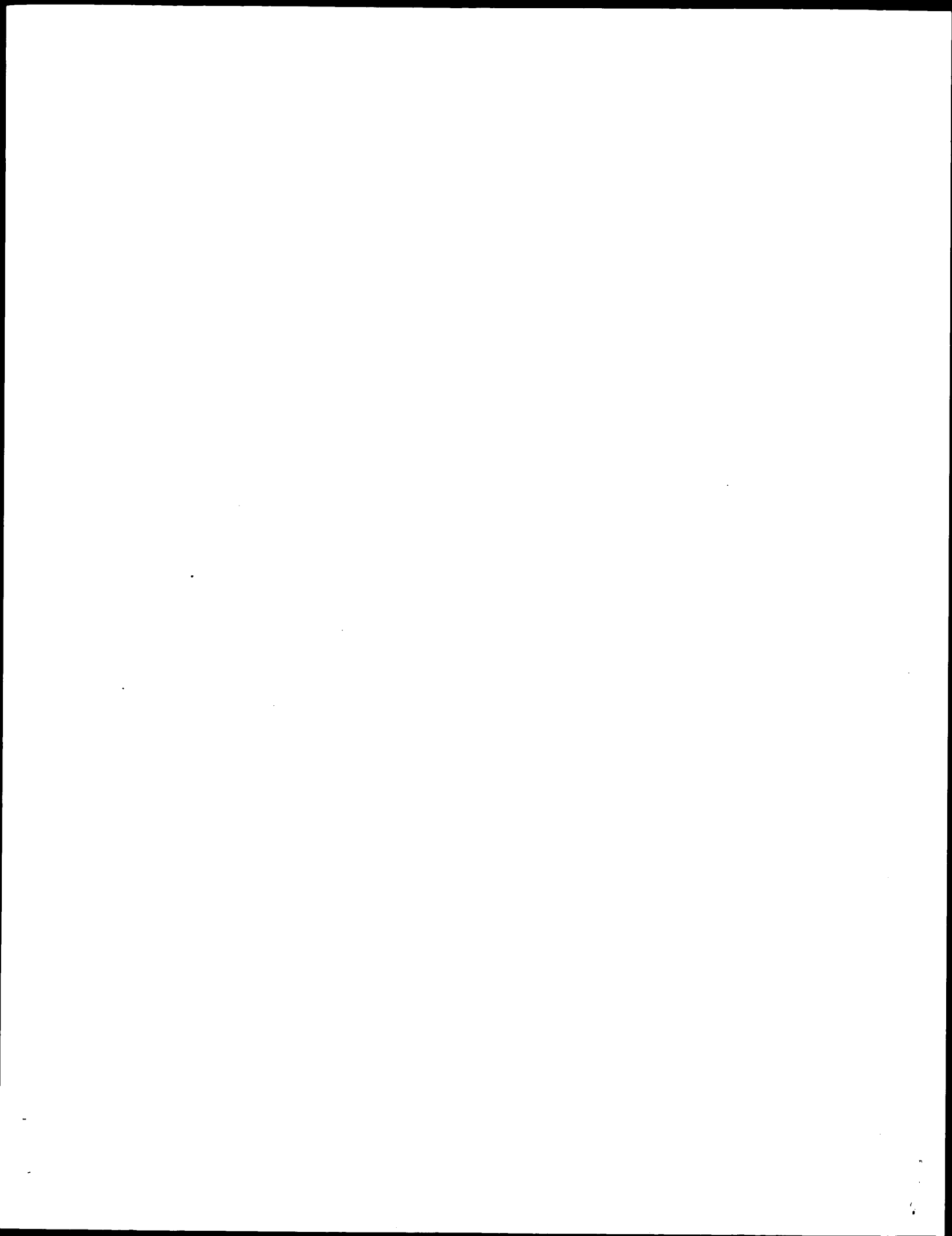
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Ddb	601	TGGTGGAGGAGCAGATTAATTTGAAAGTACACTTTGCTGAGAGCTGGAATGAAATGCCAT
Qy	661	CAC TTGCTCATAA TGGAGAATTCGGTGGAATTC TTGSGTGGTTTGATCGTTTCTGGCT
Ddb	661	CAC TTGCTCATAA TGGAGAATTCGGTGGAATTC TTGSGTGGTTTGATCGTTTCTGGCT
Qy	721	CAGCACATAGCAACCTTCTACTACTTCATGACAGTGTCTTGTATATCTTTAAGCCCTAGA
Ddb	721	CAGCACATAGCAACCTTCTACTACTTCATGACAGTGTCTTGTATATCTTTAAGCCCTAGA
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Ddb	781	ATGGCATATCACTTTTCGGAATGTGTGGAGAGTCAATGCATATGAGACTTATGATAAATTT
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Ddb	901	TATACGGAGGTGACTTGTACTTATTTGATGAGTGTCCAACAATCAAGAACTCCCAATACT
Qy	961	CGAAGACCAGTAATAGAAAACTTATACGATGTGTTGTGAACATAAGAGATGATGAAGCA
Ddb	961	CGAAGACCAGTAATAGAAAACTTATACGATGTGTTGTGAACATAAGAGATGATGAAGCA
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Ddb	1261	ATAAAGGAATAATGTGAAATTCCTTCCTGCTGCTGCTGAGAGAAATCAAAATACCCCT
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Ddb	1381	AAAAAAAAAAAAAAAA 1396

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DEFINITION	Arabidopsis thaliana IMMUTANS (IM) mRNA, nuclear gene encoding chloroplast protein, complete cds.
ACCESSION	AF098072
VERSION	AF098072.1 GI:4138854
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SOURCE	Arabidopsis thaliana.
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

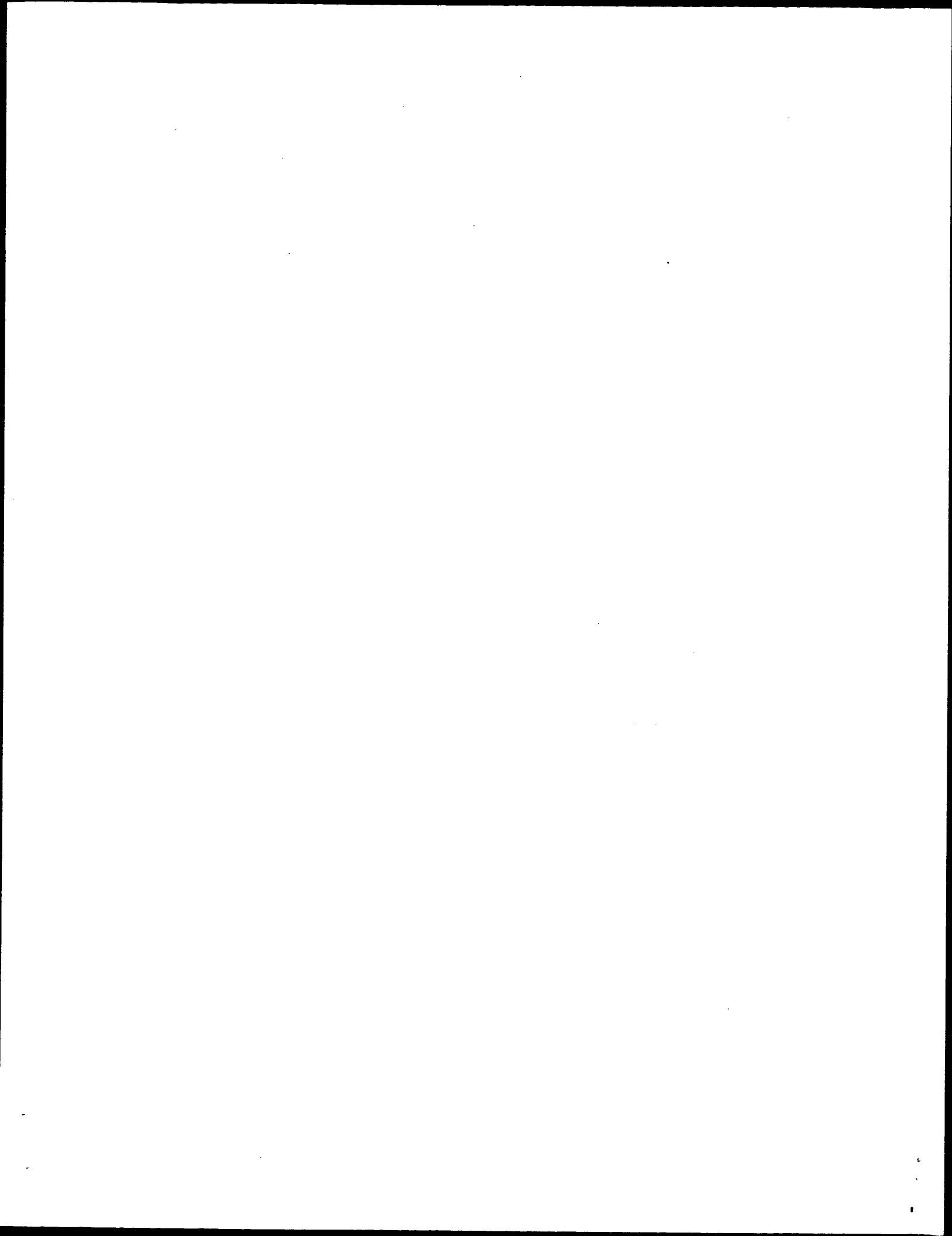
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REFERENCE 1 (bases 1 to 1448)
 AUTHORS Wu, D., Wright, D.A., Wetzel, C., Voytas, D.F. and Rodermel, S.R.
 TITLE The IMMUTANS variegation locus of Arabidopsis defines a
 early chloroplast biogenesis
 JOURNAL Plant Cell (1999) In press
 REFERENCE 2 (bases 1 to 1448)
 AUTHORS Wu, D., Wright, D.A., Wetzel, C., Voytas, D.F. and Rodermel, S.R.
 TITLE Direct Submission
 JOURNAL Submitted (09-OCT-1998) Botany, Iowa State University, 463 Bessey
 Hall, Ames, Iowa 50014, USA
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 AYHFSECVSHAYETDYKFLKASGEELKNMPPADIAKYTGDDLYLDFEFOISRTPN
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 QY 541 ATTGCTAGAGTGCCTTATTTTGCCTTTATGCTGTGTACATATGATGAGACCTTTGGT 600
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 Db 576 ATTGCTAGAGTGCCTTATTTTGCCTTTATGCTGTGTACATATGATGAGACCTTTGGT 635
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 QY 721 CAGCATAGCAACCTTCTACTTACTTCTGACAGTGTCTTGTATATCTTAAGCCCTAGA 780
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 Db 756 CAGCATAGCAACCTTCTACTTACTTCTGACAGTGTCTTGTATATCTTAAGCCCTAGA 815
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DB 241 SGEELKNMPADIAVKYITGGDLFLDFEQTSTRTNTPRPVLENLYDFVFNIRDDAEHC 300
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DB 301 KTRACOTGLSLRSPHSILDDDDTEESGCVVPEEAHCEGIVDCLKKSITS 351

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DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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DE (AT4G22260/T10114.90)
GN IM.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA;
RA Wu D., Wright D.A., Wetzel C., Voytas D.F., Rodermel S.R.;
RT "The IMUTANS variegation locus of Arabidopsis defines a mitochondrial
RT alternative oxidase homologue that functions during early chloroplast
RT biogenesis.";
RL Plant Cell 0:0-0(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Egu P., Lee J.M.,
RA Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,
RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Chao Q., Chen H., Kim C., Ecker J.;
RA "Full length cDNA sequences of Arabidopsis thaliana.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene T10114.90/AT4G22260 (GI:7269072).";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN EMBL; AF098072; AAD03599.1; -.

DR EMBL; AF326898; AAG41480.1; -;
DR EMBL; AF324563; AAG40014.1; -;
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DR InterPro; IPR002680; AOX.
DR Pfam; PF01786; AOX; 1.
KW Hypothetical protein.
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Query Match 99.8%; Score 1841; DB 10; Length 351;
Best Local Similarity 99.7%; Pred. No. 2.2e-163;
Matches 350; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MAATSGISSGTLTISRPLVTLRRSRAAVSYSSSHRLHLPLSSRLLRNHRVQATIL 60
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DB 121 DTLYRDTYARFFVLETIARVYFAFMSVLMHYETFGWRRADYLVKVFHFAESNEMHLL 180
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QY 301 KTRACOTGLSLRSPHSILDDDDTEESGCVVPEEAHCEGIVDCLKKSITS 351
DB 301 KTRACOTGLSLRSPHSILDDDDTEESGCVVPEEAHCEGIVDCLKKSITS 351

RESULT 3
O49631 PRELIMINARY; PRT; 335 AA.
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AC O49631;
DT 01-JUN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Hypothetical 38.7 kDa protein.
GN T10114.90 OR AT4G22260.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Murphy G., Drost L., Hall C., Hudson S., Ridley P.,
RA Bancroft I., Mewes H.W., Mayer K., Schueller C.;
RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL021712; CAAL6776.1; -;
DR EMBL; AL161557; CAB79181.1; -;
DR InterPro; IPR002680; AOX.
DR Pfam; PF01786; AOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 335 AA; 38674 MW; 3EE8063B73656807 CRC64;
Query Match 94.3%; Score 1739; DB 10; Length 335;
Best Local Similarity 95.2%; Pred. No. 6.8e-154;
Matches 334; Conservative 1; Mismatches 0; Indels 16; Gaps 1;
QY 1 MAATSGISSGTLTISRPLVTLRRSRAAVSYSSSHRLHLPLSSRLLRNHRVQATIL 60

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 20:54:20 : Search time 3730 Seconds
(without alignments)
10892.096 Million cell updates/sec

Title: US-09-807-867-1
Perfect score: 1396
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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 - 2: gb.htg.*
 - 3: gb.in.*
 - 4: gb.om.*
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 - 12: gb.sy.*
 - 13: gb.un.*
 - 14: gb.vi.*
 - 15: em.ba.*
 - 16: em.fun.*
 - 17: em.hum.*
 - 18: em.in.*
 - 19: em.mu.*
 - 20: em.om.*
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 - 28: em.un.*
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 - 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1302	93.3	1377	8	AY045699	AY045699 Arabidops
5	1302	93.3	1393	8	AF326898	AF326898 Arabidops
6	1054	75.5	1105	8	AF339717	AF339717 Arabidops
7	346	24.8	82891	8	ATT10114	AL021712 Arabidops
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9	70	5.0	121	6	AX325052	AX325052 Sequence
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12	70	5.0	121	6	AX325059	AX325059 Sequence
13	70	5.0	121	6	AX325060	AX325060 Sequence
14	70	5.0	121	6	AX325063	AX325063 Sequence
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22	32	2.3	1499	9	BC017387	BC017387 Homo sapi
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24	32	2.3	2267	8	LES306631	AJ308631 Lycopersi
25	32	2.3	2774	8	AF412039	AF412039 Bambusa o
26	32	2.3	20907	2	AC115584	AC115584 Dictyoste
27	32	2.3	160874	2	AC102677	AC102677 Mus muscu
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30	32	2.3	178097	2	AC016704	AC016704 Homo sapi
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32	32	2.3	206919	2	AC094991	AC094991 Rattus no
33	32	2.3	253136	2	AC095267	AC095267 Rattus no
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35	32	2.3	253305	3	PFMAL3P7	AL034559 Plasmodi
36	31	2.2	800	9	AB061546	AB061546 Homo sapi
37	31	2.2	921	6	AX364305	AX364305 Sequence
38	31	2.2	982	17	BC017415	BC017415 Homo sapi
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42	31	2.2	1560	9	BC019823	BC019823 Homo sapi
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ALIGNMENTS

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LOCUS Arabidopsis thaliana mRNA for Immunans protein.
DEFINITION
ACCESSION AJ004881
VERSION AJ004881.1 GI:3929646
KEYWORDS Immunans protein.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 1396)
AUTHORS Carol P.
TITLE Direct Submission

JOURNAL Submitted (18-MAR-1998) Carol P., Genetique Moleculaire des
Plantes, Universite Joseph Fourier, Cermo, 460 rue de la Piscine,
Saint Martin d'heres, 38053, FRANCE

REFERENCE 2 (bases 1 to 1396)

AUTHORS Carol.P., Stevenson,D., Kuntz,M., Coupland,G. and Mache,R.

TITLE The immutans locus of arabidopsis encodes a chloroplast alternative
oxidase-like protein involved in phytoene desaturation

JOURNAL Plant Cell

FEATURES Location/Qualifiers

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RADYLVKHFASNMHEMLHLLIMEELGNSWDFRELAQIATFYFYTFVFLYLSPRM
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TRRPVENLDYDFVNTRDDAEHCKTMRACQTLGSLRSPHSILDODDTEESGCVVPE
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BASE COUNT 417 a 261 c 294 g 424 t

ORIGIN

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Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1396;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db 1 CCGCTCACATGGGATTCGTATCTTCTTCTTAAACCCGCAAAATTCCTCCATTTCTAC 60

Qy 61 CAAATAATCCAACTTTTACATTTCTTCTCGTGAAATTAATCTGCTCAATCTTTGGTTC 120

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Qy 121 CTGACGGAGATGGCGGATTCAGGCATCTCCCTGGTAGCTAGCTTTACAGATTTACGGGCT 180

Db 121 CTGACGGAGATGGCGGATTCAGGCATCTCCCTGGTAGCTAGCTTTACAGGCT 180

Qy 181 TTGGTTACTCTTCGAGCTCTAGAGCCGCGTTTCGTACAGCTCCTCTCACCGATTGCTT 240

Db 181 TTGGTTACTCTTCGAGCTCTAGAGCCGCGTTTCGTACAGCTCCTCTCACCGATTGCTT 240

Qy 241 CATCATCTTCCTCTCTCTCTCGTCGTCTGCTATTAGGAACAATCATCGAGTCCAAGCA 300

Db 241 CATCATCTTCCTCTCTCTCTCGTCGTCTGCTATTAGGAACAATCATCGAGTCCAAGCA 300

Qy 301 ACGATTTTCCAGACGATGAAGAAAGCTGCTGGTGAGGAATCGTTTAAAGCCGAGACT 360

Db 301 ACGATTTTCCAGACGATGAAGAAAGCTGCTGGTGAGGAATCGTTTAAAGCCGAGACT 360

Qy 361 TCTACTGGTACAGAACCACTTGAGGAGCCAAATATGAGTTCTTCTTCACTAGTGCCTTT 420

Db 361 TCTACTGGTACAGAACCACTTGAGGAGCCAAATATGAGTTCTTCTTCACTAGTGCCTTT 420

Qy 421 GAGACATGGATCATCAAGCTTGAAGCAAGAGTGAATGTTTCTTACAGACTCGGTTATT 480

Db 421 GAGACATGGATCATCAAGCTTGAAGCAAGAGTGAATGTTTCTTACAGACTCGGTTATT 480

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541 ATTGCTAGAGTGCCTTATTTTGCGTTTATATGCTCTGCTGCTACATATGATGAGACCTTTGCT 600

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 20:54:20 ; Search time 3730 Seconds
(without alignments)
10892.096 Million cell updates/sec

Title: US-09-807-867-1

Perfect score: 1396

Sequence: 1 ccgtccacattgggttcgt.....aaaaaaaaaaaaaaaaaaaa 1396

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

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10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_ru.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

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29: em_vl.*

30: em_htg_hum.*

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32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_fod.*

36: em_htg_mam.*

37: em_htg_vrt.*

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39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	1396	100.0	1396	8	ATJ004881	Arabidops
2	1320	94.6	1448	8	AF098072	Arabidops
3	1302	93.3	1377	8	AF324663	Arabidops
4	1302	93.3	1377	8	AY045699	Arabidops
5	1302	93.3	1393	8	AF326898	Arabidops
6	1054	75.5	1105	8	AF339717	Arabidops
c 7	346	24.8	82891	8	ATT10114	Arabidops
c 8	70	5.0	121	6	AX325051	Sequence
c 9	70	5.0	121	6	AX325052	Sequence
c 10	70	5.0	121	6	AX325055	Sequence
c 11	70	5.0	121	6	AX325056	Sequence
c 12	70	5.0	121	6	AX325059	Sequence
c 13	70	5.0	121	6	AX325060	Sequence
c 14	70	5.0	121	6	AX325063	Sequence
c 15	70	5.0	121	6	AX325064	Sequence
c 16	70	5.0	121	6	AX325067	Sequence
c 17	70	5.0	121	6	AX325068	Sequence
c 18	33	2.4	1694	9	BC032406	Homo sapi
c 19	33	2.4	53045	9	AL136170	Human DNA
c 20	33	2.4	188864	2	AC125664	Rattus no
c 21	32	2.3	581	9	BC020763	Homo sapi
c 22	32	2.3	1499	9	BC017387	Homo sapi
c 23	32	2.3	1920	3	PFGTUB	X62393 P.falci
c 24	32	2.3	2267	8	LES306631	Lycopersi
c 25	32	2.3	2774	8	AF412039	Bambusa o
c 26	32	2.3	20907	2	AC115584	Dictyoste
c 27	32	2.3	160874	2	AC102677	Mus muscu
c 28	32	2.3	163229	9	AC115085	Homo sapi
c 29	32	2.3	172223	2	AC115985	Homo sapi
c 30	32	2.3	178097	2	AC016704	Homo sapi
c 31	32	2.3	204252	2	AC112392	Rattus no
c 32	32	2.3	206919	2	AC094991	Rattus no
c 33	32	2.3	253136	2	AC095267	Rattus no
c 34	32	2.3	253305	3	PFMAL3P7	Plasmodiu
c 35	32	2.3	253305	3	PFMAL3P7	Plasmodiu
c 36	31	2.2	800	9	AB061546	Homo sapi
c 37	31	2.2	921	6	AX364305	Sequence
c 38	31	2.2	982	17	BC017415	Homo sapi
c 39	31	2.2	1247	8	PSPCHS1	X63333 P.sativu
c 40	31	2.2	1393	9	BC014380	Homo sapi
c 41	31	2.2	1447	3	AF262400	Entamoeba
c 42	31	2.2	1560	9	BC019823	Homo sapi
c 43	31	2.2	1617	9	AF187859	Homo sapi
c 44	31	2.2	1848	8	AF012862	Petrossell
c 45	31	2.2	2160	9	BC015995	Homo sapi

ALIGNMENTS

RESULT 1
ATJ004881
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

ATJ004881
Arabidopsis thaliana mRNA for Immunans protein.
AJ004881
AJ004881.1 GI:3929646
Immunans protein.
thale cress.
Arabidopsis thaliana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1396)
Carol, P.
Direct Submission

1396 bp mRNA linear PLN 27-NOV-1998

Pred. No. is the number of results predicted by chance to have a

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Db	961	AATCTATACGATGTTTGTGAACATAGAGATGATGAAGCAGAACACTCGAAGCAATG	1020
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Db	1021	AGAGCTTCAGACTCAGGAGCTGCTGCTCCACACTCCATTTAGAGATGATGAT	1080
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VERSION	AY045699.1	GI:15010795	
KEYWORDS	FLI CDNA.		
SOURCE	Arabidopsis thaliana.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Kim, C.J., Chen, H., Cheuk, R., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Gibson, H.A., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.		
AUTHORS	Arabidopsis cDNA clones		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1377)		
AUTHORS	Kim, C.J., Chen, H., Cheuk, R., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Gibson, H.A., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (06-JUL-2001) Salk Institute Genomic Analysis Laboratory (SIGAL), Plant Biology Laboratory, The Salk Institute for		

USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEN (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Kim, C.J., Chen, H., Cheuk, R., Koesema, E., Meyers, M.C., Shinn, P., Banh, J., Bowser, L., Dale, J.M., Gibson, H.A., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.

Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES

Location/Qualifiers

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3'UTR 394 a 261 c 295 g 427 t
BASE COUNT
ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;

Matches 1352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 79 ACTTTTCTTCTTAAACCCGCAAAATTTCTCCATTTCACCAAAATATCCAATTTT 138

Db 61 ACTTTTCTTCTTAAACCCGCAAAATTTCTCCATTTCACCAAAATATCCAATTTT 120

QY 139 ATTTTCAGGCATCTCTCTGTTAGCTTTCAGCATTTTCACGGCTTTTGGTTACTCTTCGACGC 198

Db 121 ATTTTCAGGCATCTCTCTGTTAGCTTTCAGCATTTTCACGGCTTTTGGTTACTCTTCGACGC 180

QY 199 TCTAGAGCCGCGTTTCGTACAGCTCTCTACAGGATTGTTTCATCATCTTCTCTCTCT 258

Db 181 TCTAGAGCCGCGTTTCGTACAGCTCTCTACAGGATTGTTTCATCATCTTCTCTCTCT 240

QY 259 TCTCGTCTGCTGCTATTAAAGCAACATCATCGAGTCCCAAGCAAGGATTTTGCAGACGAT 318

Db 241 TCTCGTCTGCTGCTATTAAAGCAACATCATCGAGTCCCAAGCAAGGATTTTGCAGACGAT 300

QY 319 GAAGAGAAAGTGGTGGAGGAATCGTTTAAAGCCGAGACTTCTACTGGTACAGAACCA 378

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RESULT 5

AF326898

LOCUS

DEFINITION

Arabidopsis thaliana unknown protein (At4g22260) mRNA, complete
1393 bp mRNA linear PLN 23-APR-2002

cds.

AF326898
AF326898.1 GI:11908101
FLI_CDNA.

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Rosidae; Magnoliophyta; eudicotyledons; core eudicots;

Spermatidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1 (bases 1 to 1393)

Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,

Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L.,

Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,

Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,

Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T.,

Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K.,

Davis, R.W., Ecker, J.R. and Theologis, A.

Arabidopsids Full Length cDNA Clones

2 (bases 1 to 1393)

Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,

Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L.,

Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,

Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,

Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T.,

Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K.,

Davis, R.W., Ecker, J.R. and Theologis, A.

Direct Submission

Submitted (07-DEC-2000) Plant Gene Expression Center, 800 Buchanan

Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the

collection and clustering of RAFL cDNAs (RAFL CDNA: 'RIKEN

Arabidopsids Full-Length cDNA): Seki, M., Narusaka, M., Ishida, J.,

Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,

Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the

sequencing and annotation of the RAFL cDNAs: Yamada, K., Liu, S.X.,

Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D.,

Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Chen, H.,

Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J.,

Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A.,

Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to

this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC)

contributed equally to this work as PIs.

Location/Qualifiers

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ORIGIN

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Qy 1159 TGCCTCAAGAAATCCATTAACAAGTTTAATAAATAGAACTAAACTAAAAAAGATTATTG 1218
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Qy 1279 ATTCCCATCGTTGCTAGTGTGTGAGAGAATCAAAATACCTAATGATGATGATGATGAT 1338
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Qy 1339 TGATGAGCTTAAGTCTGTTGTAGACCATTTTATC 1371
Db 1321 TGATGAGCTTAAGTCTGTTGTAGACCATTTTATC 1353

RESULT 6

AF339717

LOCUS

DEFINITION

AF339717

VERSION

AF339717.1

KEYWORDS

FLI_CDNA.

SOURCE

Arabidopsis thaliana.

ORGANISM

Arabidopsis thaliana.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 1105)

AUTHORS

Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Etgu, P., Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H., Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.

TITLE

Arabidopsis Open Reading Frame (ORF) Clones

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 1105)

AUTHORS

Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

DIRECT SUBMISSION

Submitted (24-JAN-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGECC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAPL cDNAs: Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B.,


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Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1335 ACTTTGATGAGCTTAAGTCGTTGTAGACATTTTATC 1371
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RESULT 8
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DEFINITION Sequence 1189 from Patent W00192512.
ACCESSION AX325051
VERSION    AX325051.1 GI:18095806
KEYWORDS   thale cress.
SOURCE     Arabidopsis thaliana
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

AUTHORS    Kmiec,E.B., Camper,H.B., Rice,M.C. and Kim,J.
TITLE      Targeted chromosomal genomic alterations in plants using modified
            single stranded oligonucleotides
JOURNAL    Patent: WO 0192512-A 1189 06-DEC-2001;
            UNIVERSITY OF DELAWARE (US)
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VERSION    AX325052.1 GI:18095807
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

AUTHORS    Kmiec,E.B., Camper,H.B., Rice,M.C. and Kim,J.
TITLE      Targeted chromosomal genomic alterations in plants using modified
            single stranded oligonucleotides
JOURNAL    Patent: WO 0192512-A 1190 06-DEC-2001;
            UNIVERSITY OF DELAWARE (US)
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SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1193 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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DEFINITION Sequence 1194 from Patent WO0192512.
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VERSION AX325056.1 GI:18095811
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SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1194 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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VERSION AX325059.1 GI:18095814
KEYWORDS thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1197 06-DEC-2001;
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KEYWORDS thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1198 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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Db 1 G 1

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VERSION AX325063.1 GI:18095818
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SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1
AUTHORS Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1201 06-DEC-2001;
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ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1
AUTHORS Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1201 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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ACCESSION AX325064
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SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1
AUTHORS Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1202 06-DEC-2001;
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Copyright (c) 1993 - 2003 CompuGen Ltd.

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XX 26-JAN-2001; 2001US-0770445.
XX 27-JAN-2000; 2000US-178472P.
XX (GORL/) GORLACH J.
PA (ANYX/) AN Y.
PA (HAML/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
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PA (HURB/) HURBAN P.
XX Goriach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX WPI: 2002-400781/43.
XX New Arabidopsis thaliana nucleic acid for identifying homologous genes,
PT producing compositions that modulate the expression or function of its
PT encoded protein, and mapping functional regions of protein -
XX Claim 1: SEQ ID NO 418; 49pp + Sequence Listing; English.
XX The invention relates to an Arabidopsis thaliana nucleic acid (I)
CC comprising a sequence capable of hybridising under stringent conditions
CC to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
CC given in the specification or its fragment. A polypeptide (II) encoded by
CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
CC genetically modified cell (IV) comprising an exogenous nucleic acid, is
CC useful for screening a candidate agent for its biological effect. (I) is
CC useful in identifying homologous or related genes, in producing
CC compositions that modulate the expression or function of its encoded
CC protein, mapping functional regions of the protein and in studying
CC associated physiological pathways. (I) is also useful for the genetic
CC manipulation of cells, particularly plant cells. (I) is also useful in
CC screening assays of various plant strains to determine the strains that
CC are best capable of withstanding a particular disease or environmental
CC stress. (II) and (III) are useful for screening of biologically active
CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
CC pathways. The screened agents are useful in improved methods of treating
CC crops to prevent or treat disease. (II) are also useful in screening
CC programs to identify agents that mimic or enhance the action of tolerance
CC factors. Such agents are useful in improved methods of treating crops to
CC enhance their tolerance to environmental stress. (I) is also useful
CC for enhancing or inhibiting production of a biosynthetic product in a
CC plant. (III) is useful for identifying other mediators that may induce
CC expression of proteins of interest, for establishing the extent to which
CC any specific insect and/or pathogen is responsible for damage to a
CC particular plant, for identifying other mediators that enhance or induce
CC tolerance to environmental stress, for identifying factors involved in
CC biosynthetic pathways of nutritional, commercial, or medicinal value and
CC for identifying productions of nutritional, commercial or medicinal
CC value. (IV) is useful in the study of genetic function and regulation,
CC for alteration of the cellular metabolism and for screening compounds
CC that may affect the biological function of the gene or gene products.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=999909770445.
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DB 441 CGGATATCGCAGTAAATACTATACGGGAGTGACTTGTACTTATTGATGAGTTCCTCAA 382
QY 941 CATCAAGAACTCCCAATACTCGAAGACCAGTAAAGAAAATCATACGATGTTGTGTA 1000
DB 381 CATCAAGAACTCCCAATACTCGAAGACCAGTAAAGAAAATCATACGATGTTGTGTA 322
QY 1001 ACATAGAGATCATGAAGCAGAACACTGCAACACATGAGAGCTTGTGAGAGTCTAGGCA 1060
DB 321 ACATAGAGATCATGAAGCAGAACACTGCAACACATGAGAGCTTGTGAGAGTCTAGGCA 262
QY 1061 GTCTCGGTTCTCCACACTCCATTTTAGATGATGATGATGATGATGATGATGATGATGATG 1120
DB 261 GTCTCGGTTCTCCACACTCCATTTTAGATGATGATGATGATGATGATGATGATGATG 202
QY 1121 TTGTTCTCGAGAGGCTCATTCGGAAGGTATTTGTAGACTGCCTCAAGAAATCCATTACAA 1180
DB 201 TTGTTCTCGAGAGGCTCATTCGGAAGGTATTTGTAGACTGCCTCAAGAAATCCATTACAA 142
QY 1181 GTTAATAAATAGAAAGTAAACTAAAAAGATTTATTTGTATCAGCTCATGAACAATAGAT 1240
DB 141 GTTAATAAATAGAAAGTAAACTAAAAAGATTTATTTGTATCAGCTCATGAACAATAGAT 82
QY 1241 ATAATCCCATATCTTTGGGAATAAAGGAATAATGTCAAAATCCCATCGTGTGTAGTGT 1300
DB 81 ATAATCCCATATCTTTGGGAATAAAGGAATAATGTCAAAATCCCATCGTGTGTAGTGT 22
QY 1301 GTGAGAGAAATCAAAATACCCCTA 1321
DB 21 GTGAGAGAAATCAAAATACCCCTA 1

CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.

XX Sequence 121 BP; 43 A; 29 C; 29 G; 20 T; 0 other;

Query Match 5.0%; Score 70; DB 24; Length 121;
Best Local Similarity 99.2%; Pred. No. 3.4e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 83 TTCCTTCCTGCAATATCTGCTCAAAATCTTGGTTCCTGACGAGATGCGCGGATTT 142

Db 121 TCTTTCTCTGAAATATCTGCTCAAAATCTTGGTTCCTGACGAGATGCGCGGATTT 62

QY 143 CAGGCATCTCCTCTGGTACGTGAGATTTTCACGGCCCTTGGTTACTCTTCGAGGCTCTA 202

Db 61 GAGGCATCTCCTCTGGTACGTGAGATTTTCACGGCCCTTGGTTACTCTTCGAGGCTCTA 2

QY 203 G 203

Db 1 G 1

RESULT 5

ABK25833

ID ABK25833 standard; DNA; 121 BP.

XX

AC ABK25833;

DT 09-APR-2002 (first entry)

XX Albino plant producing genome altering oligonucleotide #5.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.

XX Arabidopsis thaliana.

OS Synthetic.

XX WO200192512-A2.

XX

XX 06-DEC-2001.

XX 01-JUN-2001; 2001WO-US17672.

XX 01-JUN-2000; 2000US-208538P.

PR 30-OCT-2000; 2000US-244989P.

PR 27-MAR-2001; 2001US-0818875.

XX

PA (UYDE) UNIV DELAWARE.

XX Kmiec EB, Gamber HB, Rice MC, Kim J;

XX WPI; 2002-106307/14.

XX New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production -

XX Claim 7; Page 115; 220pp; English.

XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.

XX Sequence 121 BP; 20 A; 34 C; 31 G; 36 T; 0 other;

Query Match 5.0%; Score 70; DB 24; Length 121;

Best Local Similarity 99.2%; Pred. No. 3.4e-18;

Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 104 GCTCAATCTTTGGTTCTGACGAGATGCGCGGATTTTCAGGCATCTCTCTGTTACGT 163

Db 1 GCTCAATCTTTGGTTCTGACGAGATGCGCGGATTTTCAGGCATCTCTCTGTTACGT 60

QY 164 TGACGATTTACGGCCCTTTGGTTACTCTTCGACGCTCTAGAGCCGCGTTTCGTACAGCT 223

Db 61 AGACGATTTACGGCCCTTTGGTTACTCTTCGACGCTCTAGAGCCGCGTTTCGTACAGCT 120

QY 224 C 224

Db 121 C 121

RESULT 6

ABK25834/C

ID ABK25834 standard; DNA; 121 BP.

XX

AC ABK25834;

XX 09-APR-2002 (first entry)

XX Albino plant producing genome altering oligonucleotide #6.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;

KW	modified oil production; modified starch production; waxy starch;
KW	altered floral morphology; male-sterile plant; albino mutant;
KW	modified fatty acid content; reduced palmitate production; albino plant;
KW	increased stearate production; reduced linolenic acid production;
KW	photosynthetic process.
XX	
OS	Arabidopsis thaliana.
OS	Synthetic.
XX	
PN	WO200192512-A2.
XX	
PD	06-DEC-2001.
XX	
PF	01-JUN-2001; 2001WO-US17672.
XX	
PR	01-JUN-2000; 2000US-208538P.
PR	30-OCT-2000; 2000US-244989P.
PR	27-MAR-2001; 2001US-0818875.
XX	
PA	(UYDE) UNIV DELAWARE.
XX	
PL	Kmiec EB, Gamper HB, Rice MC, Kim J;
XX	
DR	WPI; 2002-106307/14.
XX	
PT	New oligonucleotides with modified nuclease-resistant termini, useful
PT	for creating plants with desired phenotypes, e.g. stress tolerance,
PT	improved nutritional value, herbicide or disease resistance, or
PT	modified oil production
XX	
FS	Claim 7; Page 115; 220pp; English.
XX	
CC	The invention relates to an oligonucleotide for targeted alteration of a
CC	genetic sequence, which comprises a single-stranded oligonucleotide
CC	having a DNA domain. The DNA domain has at least one mismatch with
CC	respect to the genetic sequence to be altered and further comprises
CC	chemical modifications of the oligonucleotide. The chemical modifications
CC	consist of o-methyl modification, an LNA modification, two or more
CC	phosphorothioate linkages on a terminus, or a combination of any two or
CC	more of these modifications. The oligonucleotides are useful for
CC	directing repair or alteration of plant genetic information. The
CC	oligonucleotides are particularly useful for creating plants with desired
CC	phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC	nutritional value (e.g. altering amino acid content of plants or
CC	confering amino acid over production), herbicide resistance (e.g.
CC	glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC	resistance, porphyrin herbicide resistance or triazine resistance),
CC	disease resistance, modified oil production, modified starch production
CC	(e.g. increased starch or production of waxy starch), altered floral
CC	morphology (e.g. male-sterile plants) or modified fatty acid content
CC	(e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC	The oligonucleotides are also useful for producing albino mutants for the
CC	analysis of photosynthetic processes. This sequence represents a genome
CC	altering oligonucleotide of the invention.
XX	
SQ	Sequence 121 BP; 36 A; 31 C; 34 G; 20 T; 0 other;
	Query Match 5.0%; Score 70; DB 24; Length 121;
	Best Local Similarity 99.2%; Pred. No. 3.4e-18;
	Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	104 GCTCAATCTTGGTTCCTGACGAGATGGCGGCATTTCAGGCATCTCCCTGTCAGCT 163
Db	121 GCYCAATCTTGGTTCCTGACGAGATGGCGGCATTTCAGGCATCTCCCTGTCAGCT 62
QY	164 TGACGATTCACGGCCTTTGGTTACTCTTCGACGCTCTAGAGCGCGCTTCGTACAGCT 223
Db	61 AGACGATTCACGGCCTTTGGTTACTCTTCGACGCTCTAGAGCGCGCTTCGTACAGCT 2
QY	224 C 224
Db	1 C 1

PA (UYDE) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production -
XX
XX Claim 7; Page 115; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.
XX
XX Sequence 121 BP; 17 A; 39 C; 25 G; 40 T; 0 other;
SQ

Query Match 5.0%; Score 70; DB 24; Length 121;
Best Local Similarity 99.2%; Pred. No. 3.4e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 133 GCGGCGATTTCAGGCATCTCTCTGTTAGCTTTCAGGATTCACGGCTTTGGTTACTCTT 192
Db 1 GCGGCGATTTCAGGCATCTCTCTGTTAGCTTTCAGGATTCACGGCTTTGGTTACTCTT 60
QY 193 CGAGCTCTAGAGCCGCGCTTTCGTACAGCTCTCTACCGATTGCTTCATCATCTTCT 252
Db 61 TGACGCTCTAGAGCCGCGCTTTCGTACAGCTCTCTACCGATTGCTTCATCATCTTCT 120
QY 253 C 253
Db 121 C 121

RESULT 10
ABK25842/c
ID ABK25842 standard; DNA; 121 BP.
XX
XX AC ABK25842;
XX
XX 09-APR-2002 (first entry)
XX
XX Albino plant producing genome altering oligonucleotide #14.
XX
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;

KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
XX Arabidopsis thaliana.
OS Synthetic.
XX
XX WO200192512-A2.
XX
XX PD 06-DEC-2001.
XX
XX 01-JUN-2001; 2001WO-US17672.
XX
XX 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
PR 27-MAR-2001; 2001US-0818875.
XX
XX (UYDE) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production -
XX
XX Claim 7; Page 115; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.
XX
XX Sequence 121 BP; 40 A; 25 C; 39 G; 17 T; 0 other;
SQ

Query Match 5.0%; Score 70; DB 24; Length 121;
Best Local Similarity 99.2%; Pred. No. 3.4e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 133 GCGGCGATTTCAGGCATCTCTCTGTTAGCTTTCAGGATTCACGGCTTTGGTTACTCTT 192
Db 121 GCGGCGATTTCAGGCATCTCTCTGTTAGCTTTCAGGATTCACGGCTTTGGTTACTCTT 62
QY 193 CGAGCTCTAGAGCCGCGCTTTCGTACAGCTCTCTACCGATTGCTTCATCATCTTCT 252
Db 61 TGACGCTCTAGAGCCGCGCTTTCGTACAGCTCTCTACCGATTGCTTCATCATCTTCT 2
QY 253 C 253
Db 1 C 1

RESULT 11
ABK25845
ID ABK25845 standard; DNA: 121 BP.
XX
AC ABK25845;
XX
DT 09-APR-2002 (first entry)
XX
DE Albino plant producing genome altering oligonucleotide #17.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; triazine resistance; disease resistance;
KW porphyrin herbicide resistance; modified starch production; waxy starch;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Arabidopsis thaliana.
OS Synthetic.
XX
PN WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US17672.
XX
PR 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
PR 27-MAR-2001; 2001US-0818875.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production -
XX
PS Claim 7; Page 116; 220pp; English.
XX
CC The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.
XX
SQ Sequence 121 BP; 15 A; 42 C; 21 G; 43 T; 0 other;

Query Match 5.0%; Score 70; DB 24; Length 121;
Best Local Similarity 99.2%; Pred No. 3.4e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 142 TCAGGCATCTCCTCTGGTACGTGACGATTTTCACGGCCCTTGGTTACTCTTCGAGCTCT 201
DB 1 TCAGGCATCTCCTCTGGTACGTGACGATTTTCACGGCCCTTGGTTACTCTTCGAGCTCT 60
QY 202 AGAGCCCGCGTTTCGTACAGCTCCTCTACAGCTCCTCTACAGCTCCTCTCTCTCTCTCT 261
DB 61 TGAGCCCGCGTTTCGTACAGCTCCTCTACAGCTCCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 262 C 262
DB 121 C 121
RESULT 12
ABK25846/C
ID ABK25846 standard; DNA: 121 BP.
XX
AC ABK25846;
XX
DT 09-APR-2002 (first entry)
XX
DE Albino plant producing genome altering oligonucleotide #18.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; triazine resistance; disease resistance;
KW porphyrin herbicide resistance; modified starch production; waxy starch;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Arabidopsis thaliana.
OS Synthetic.
XX
PN WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US17672.
XX
PR 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
PR 27-MAR-2001; 2001US-0818875.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production -
XX
PS Claim 7; Page 116; 220pp; English.
XX
CC The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.
XX
SQ Sequence 121 BP; 15 A; 42 C; 21 G; 43 T; 0 other;

CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 328 BP; 139 A; 52 C; 48 G; 88 T; 1 other;
 Query Match 2.4%; Score 33; DB 23; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1364 ATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
 DB 170 ATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 202
 RESULT 15
 AAH87785/C
 ID AAH87785 standard; cDNA; 574 BP.
 XX
 AC AAH87785;
 DT 25-SEP-2001 (first entry)
 DE Peppermint plant oil gland expressed cDNA 141.
 XX
 KW Peppermint; plant oil gland cell; terpenoid essential oil; resin;
 KW genetic mapping; antisense suppression; recombinant expression; ss.
 XX
 OS Mentha x piperita.
 XX
 PN WO200153319-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 19-JAN-2001; 2001WO-US02567.
 XX
 PR 20-JAN-2000; 2000US-0177264.
 XX
 PA (CROT/) CROTEAU R B.
 PA (LANG/) LANGE B M.
 PA (WILD/) WILDUNG M R.
 XX
 PI Croteau RB, Lange BM, Wildung MR;
 XX
 DR WPI; 2001-488706/53.
 XX
 PT New nucleic acid molecules corresponding to mRNA molecules expressed in
 PT peppermint oil glands for enhancing expression of plant oil gland cell
 PT proteins -
 XX
 PS Claim 1; Page 131; 251pp; English.
 XX
 CC The invention relates to nucleic acid molecules (AAH87645-AAH88116) that
 CC correspond to all or part of a mRNA molecule expressed in plant oil
 CC gland cells, especially peppermint and plant oil glands that produce
 CC terpenoid essential oils and resins. The nucleic acids are useful for
 CC genetically mapping a plant genome for genes expressed in plant oil
 CC gland cells and to suppress (for example by antisense suppression) or
 CC enhance their expression (for example by genetically transforming a
 CC plant cell with a replicable expression vector that expresses one or more
 CC proteins naturally expressed in plant oil gland cells). The nucleic acids
 CC are also useful for recombinant expression of plant oil gland proteins
 CC required for terpenoid essential oil and/or resin production in bacterial
 CC and/or yeast cells.

XX
 SQ Sequence 574 BP; 177 A; 137 C; 113 G; 147 T; 0 other;
 Query Match 2.3%; Score 32; DB 22; Length 574;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1364 ATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1395
 DB 32 ATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
 Search completed: February 2, 2003, 21:01:19
 Job time : 329 secs

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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 20:07:44 : Search time 65 Seconds
(without alignments)
6586.473 Million cell updates/sec

Title: US-09-807-867-1
Perfect score: 1396
Sequence: 1 ccgctcacattggattcgt.....aaaaaaaaaaaaaaaaaaaaa 1396

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Match	Length	DB ID	Description
1	33	2.4	1739	4 US-09-594-193-1	Sequence 1, Appli
2	31	2.2	1617	4 US-09-444-336-4	Sequence 4, Appli
3	31	2.2	4337	3 US-09-187-049-1	Sequence 1, Appli
4	30	2.1	1255	4 US-09-149-476-75	Sequence 75, Appli
5	30	2.1	1448	4 US-09-387-212-12	Sequence 12, Appli
6	30	2.1	1448	4 US-09-948-802-12	Sequence 12, Appli
7	30	2.1	1622	4 US-09-334-601-9	Sequence 9, Appli
8	30	2.1	1889	3 US-08-861-747-3	Sequence 3, Appli
9	29	2.1	732	4 US-09-149-476-66	Sequence 66, Appli
10	29	2.1	1012	4 US-09-615-192A-94	Sequence 94, Appli
11	29	2.1	1026	2 US-08-713-000-6	Sequence 6, Appli
12	29	2.1	1026	2 US-08-975-316-6	Sequence 6, Appli
13	29	2.1	1026	4 US-09-211-710-6	Sequence 6, Appli
14	29	2.1	1026	4 US-09-615-192A-6	Sequence 3, Appli
15	29	2.1	1066	2 US-08-605-106-3	Sequence 3, Appli
16	29	2.1	1318	4 US-09-443-041A-25	Sequence 25, Appli
17	28	2.0	945	4 US-09-268-364-3	Sequence 3, Appli
18	28	2.0	1001	1 US-08-728-259A-10	Sequence 10, Appli
19	28	2.0	1001	2 US-08-473-486-10	Sequence 10, Appli
20	28	2.0	1098	3 US-09-248-335-35	Sequence 35, Appli
21	28	2.0	1275	3 US-08-725-532A-2	Sequence 2, Appli
22	28	2.0	1587	3 US-09-108-020-11	Sequence 11, Appli
23	28	2.0	1737	4 US-09-416-050A-7	Sequence 7, Appli
24	28	2.0	1737	4 US-09-664-800-7	Sequence 7, Appli
25	28	2.0	1737	4 US-09-665-309-7	Sequence 7, Appli
26	28	2.0	1737	4 US-09-661-569-7	Sequence 7, Appli
27	28	2.0	1957	4 US-09-352-990-11	Sequence 11, Appli

28 28 2.0 2017 4 US-09-291-922-21 Sequence 21, Appli
29 28 2.0 2158 1 US-07-602-608-1 Sequence 1, Appli
30 28 2.0 2158 1 US-08-261-578-1 Sequence 1, Appli
31 28 2.0 2606 4 US-09-234-827B-3 Sequence 3, Appli
32 28 2.0 4032 1 US-08-126-587C-8 Sequence 8, Appli
33 28 2.0 59065 4 US-09-813-817-3 Sequence 3, Appli
34 28 2.0 59065 4 US-09-978-197-3 Sequence 3, Appli
35 27 1.9 42 1 US-08-741-881-3 Sequence 3, Appli
36 27 1.9 42 1 US-08-739-158-3 Sequence 3, Appli
37 27 1.9 42 2 US-08-739-167-3 Sequence 3, Appli
38 27 1.9 42 3 US-08-404-796-3 Sequence 3, Appli
39 27 1.9 42 3 US-08-931-869-3 Sequence 3, Appli
40 27 1.9 42 4 US-09-350-399-3 Sequence 3, Appli
41 27 1.9 42 4 US-09-236-140A-3 Sequence 3, Appli
42 27 1.9 48 1 US-08-741-881-21 Sequence 21, Appli
43 27 1.9 48 1 US-08-739-158-21 Sequence 21, Appli
44 27 1.9 48 2 US-08-739-167-21 Sequence 21, Appli
45 27 1.9 48 3 US-08-404-796-21 Sequence 21, Appli

ALIGNMENTS

RESULT 1
US-09-594-193-1
; Sequence 1, Application US/09594193
; Patent No. 6441274
; GENERAL INFORMATION:
; APPLICANT: CAHOON, REBECCA E.
; APPLICANT: FALCO, S. CARL
; TITLE OF INVENTION: NOVEL PLANT TRYPTOPHAN SYNTHASE BETA SUBUNIT
; FILE REFERENCE: B1374 US NA
; CURRENT APPLICATION NUMBER: US/09/594,193
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,568
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1739
; TYPE: DNA
; ORGANISM: Zea mays
US-09-594-193-1

Query Match 2.4%; Score 33; DB 4; Length 1739;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1364 ATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
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Db 1701 ATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1733

RESULT 2
US-09-444-336-4
; Sequence 4, Application US/09444336
; Patent No. 6410713
; GENERAL INFORMATION:
; APPLICANT: Guerriero, Vincent
; APPLICANT: Raynes, Deborah A
; TITLE OF INVENTION: DNA Encoding Proteins That Inhibit Hsp70 Function
; FILE REFERENCE: HspBP DNA and Protein Sequences
; CURRENT APPLICATION NUMBER: US/09/444,336
; CURRENT FILING DATE: 1999-11-19
; EARLIER APPLICATION NUMBER: 60/109,351
; EARLIER FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-444-336-4

Query Match 2.2%; Score 31; DB 4; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 31; Conservative 0; Mismatches 0; Indels

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Db	1587	TTTATCAAAAAAAAAAAAAAAAAA	1617

RESULT. T 3

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12-0001
US-09/187-049-1
; Sequence 1, Application US/09187049
; Patent No. 6117666
; GENERAL INFORMATION:
; APPLICANT: Lamppa, Gayle K.
; TITLE OF INVENTION: PLASTID PROTEOLYTIC PROCESSING ENZYME
; THAT CLEAVES PRECURSOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BRINKS HOFER GILSON & LIONE
; STREET: P. O. Box 10395
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187-049

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Query Match 2.2%; Score 31; DB 3; Length 4337;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 31; Conservative 0; Mismatches 0; Indels

QY	1366	TTTATCAAAAAAAAAAAAAAAAAAAAAA	1396
Db	4302	TTTATCAAAAAAAAAAAAAAAAAAAAAA	4332

RESULT 4

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US-09/149-476-75
US-09/149-476-75
; Sequence 75, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476

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1	EARLIER APPLICATION NUMBER: 60/043,674	2	EARLIER FILING DATE: 1937-04-11	3	EARLIER APPLICATION NUMBER: 60/043,669	4	EARLIER FILING DATE: 1937-04-11	5	EARLIER APPLICATION NUMBER: 60/043,312	6	EARLIER FILING DATE: 1937-04-11	7	EARLIER APPLICATION NUMBER: 60/043,313	8	EARLIER FILING DATE: 1937-04-11	9	EARLIER APPLICATION NUMBER: 60/043,672	10	EARLIER FILING DATE: 1937-04-11	11	EARLIER APPLICATION NUMBER: 60/043,315	12	EARLIER FILING DATE: 1937-04-11	13	EARLIER APPLICATION NUMBER: 60/048,974	14	EARLIER FILING DATE: 1937-06-06	15	EARLIER APPLICATION NUMBER: 60/056,886	16	EARLIER FILING DATE: 1937-08-22	17	EARLIER APPLICATION NUMBER: 60/056,877	18	EARLIER FILING DATE: 1937-08-22	19	EARLIER APPLICATION NUMBER: 60/056,889	20	EARLIER FILING DATE: 1937-08-22	21	EARLIER APPLICATION NUMBER: 60/056,893	22	EARLIER FILING DATE: 1937-08-22	23	EARLIER APPLICATION NUMBER: 60/056,630	24	EARLIER FILING DATE: 1937-08-22	25	EARLIER APPLICATION NUMBER: 60/056,878	26	EARLIER FILING DATE: 1937-08-22	27	EARLIER APPLICATION NUMBER: 60/056,662	28	EARLIER FILING DATE: 1937-08-22	29	EARLIER APPLICATION NUMBER: 60/056,872	30	EARLIER FILING DATE: 1937-08-22	31	EARLIER APPLICATION NUMBER: 60/056,882	32	EARLIER FILING DATE: 1937-08-22	33	EARLIER APPLICATION NUMBER: 60/056,637	34	EARLIER FILING DATE: 1937-08-22	35	EARLIER APPLICATION NUMBER: 60/056,903	36	EARLIER FILING DATE: 1937-08-22	37	EARLIER APPLICATION NUMBER: 60/056,888	38	EARLIER FILING DATE: 1937-08-22	39	EARLIER APPLICATION NUMBER: 60/056,879	40	EARLIER FILING DATE: 1937-08-22	41	EARLIER APPLICATION NUMBER: 60/056,880	42	EARLIER FILING DATE: 1937-08-22	43	EARLIER APPLICATION NUMBER: 60/056,894	44	EARLIER FILING DATE: 1937-08-22	45	EARLIER APPLICATION NUMBER: 60/056,911	46	EARLIER FILING DATE: 1937-08-22	47	EARLIER APPLICATION NUMBER: 60/056,636	48	EARLIER FILING DATE: 1937-08-22	49	EARLIER APPLICATION NUMBER: 60/056,874	50	EARLIER FILING DATE: 1937-08-22	51	EARLIER APPLICATION NUMBER: 60/056,910	52	EARLIER FILING DATE: 1937-08-22	53	EARLIER APPLICATION NUMBER: 60/047,595	54	EARLIER FILING DATE: 1937-05-23	55	EARLIER APPLICATION NUMBER: 60/047,599	56	EARLIER FILING DATE: 1937-05-23	57	EARLIER APPLICATION NUMBER: 60/047,588	58	EARLIER FILING DATE: 1937-05-23	59	EARLIER APPLICATION NUMBER: 60/047,585	60	EARLIER FILING DATE: 1937-05-23	61	EARLIER APPLICATION NUMBER: 60/047,586	62	EARLIER FILING DATE: 1937-05-23	63	EARLIER APPLICATION NUMBER: 60/047,590	64	EARLIER FILING DATE: 1937-05-23
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7	EARLIER	FILING DATE:	1997-05-23
7	EARLIER	APPLICATION NUMBER:	60/047,594
7	EARLIER	FILING DATE:	1997-05-23
7	EARLIER	APPLICATION NUMBER:	60/047,589
7	EARLIER	FILING DATE:	1997-05-23
7	EARLIER	APPLICATION NUMBER:	60/047,593
7	EARLIER	FILING DATE:	1997-05-23
7	EARLIER	APPLICATION NUMBER:	60/047,614
7	EARLIER	FILING DATE:	1997-05-23
7	EARLIER	APPLICATION NUMBER:	60/043,578
7	EARLIER	FILING DATE:	1997-04-11
7	EARLIER	APPLICATION NUMBER:	60/043,576
7	EARLIER	FILING DATE:	1997-04-11
7	EARLIER	APPLICATION NUMBER:	60/047,501
7	EARLIER	FILING DATE:	1997-05-23
7	EARLIER	APPLICATION NUMBER:	60/043,670
7	EARLIER	FILING DATE:	1997-04-11
7	EARLIER	APPLICATION NUMBER:	60/056,632
7	EARLIER	FILING DATE:	1997-08-22
7	EARLIER	APPLICATION NUMBER:	60/056,664
7	EARLIER	FILING DATE:	1997-08-22
7	EARLIER	APPLICATION NUMBER:	60/056,876
7	EARLIER	FILING DATE:	1997-08-22
7	EARLIER	APPLICATION NUMBER:	60/056,881
7	EARLIER	FILING DATE:	1997-08-22
7	EARLIER	APPLICATION NUMBER:	60/056,909
7	EARLIER	FILING DATE:	1997-08-22
7	EARLIER	APPLICATION NUMBER:	60/056,875
7	EARLIER	FILING DATE:	1997-08-22
7	EARLIER	APPLICATION NUMBER:	60/056,862
7	EARLIER	FILING DATE:	1997-08-22
7	EARLIER	APPLICATION NUMBER:	60/056,887
7	EARLIER	FILING DATE:	1997-08-22
7	EARLIER	APPLICATION NUMBER:	60/056,908
7	EARLIER	FILING DATE:	1997-08-22
7	EARLIER	APPLICATION NUMBER:	60/048,964
7	EARLIER	FILING DATE:	1997-06-06
7	EARLIER	APPLICATION NUMBER:	60/057,650
7	EARLIER	FILING DATE:	1997-09-05
7	EARLIER	APPLICATION NUMBER:	60/056,884
7	EARLIER	FILING DATE:	1997-08-22
7	EARLIER	APPLICATION NUMBER:	60/057,669
7	EARLIER	FILING DATE:	1997-09-05
7	EARLIER	APPLICATION NUMBER:	60/049,610
7	EARLIER	FILING DATE:	1997-06-13
7	EARLIER	APPLICATION NUMBER:	60/061,060
7	EARLIER	FILING DATE:	1997-10-02

Query Match 2.1%; Score 30; DB 4; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 30; Conservative 0; Mismatches 0; Indels

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAA 1396
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 Db 1192 TTATCAAAAAAAAAAAAAAAAAAAAA 1221

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RESULT 5
US-09-387-212-12
; Sequence 12, Application US/09387212A
; Patent No. 6309849
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/09/387.212A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1448
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurrences of n indicate any nucleotide
US-09-387-212-12

Query Match 2.1%; Score 30; DB 4; Length 1448;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
Db 1223 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1252

RESULT 6

US-09-948-802-12
; Sequence 12, Application US/09948802
; Patent No. 6465232
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/09/948,802
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387,212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurrences of n indicate any nucleotide
US-09-948-802-12

Query Match 2.1%; Score 30; DB 4; Length 1448;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
Db 1223 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1252

RESULT 7

US-09-334-601-9
; Sequence 9, Application US/09334601
; Patent No. 6280989
; GENERAL INFORMATION:
; APPLICANT: Kapitonov, Dmitri
; APPLICANT: Yu, Robert
; TITLE OF INVENTION: NOVEL STIALYLTRANSFERASES
; FILE REFERENCE: VCUIP-6
; CURRENT APPLICATION NUMBER: US/09/334,601
; CURRENT FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1622
; TYPE: DNA
; ORGANISM: Murinae gen. sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (498)..(1484)
US-09-334-601-9

Query Match 2.1%; Score 30; DB 4; Length 1622;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396

Db 1586 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1615

RESULT 8

US-08-861-747-3
; Sequence 3, Application US/08861747
; Patent No. 6020158
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G.
; APPLICANT: VYAS, Tejal B.
; TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 15th St., NW, Suite 330 - G Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,747
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jahns, Kristina M.
; REGISTRATION NUMBER: 41,092
; REFERENCE/DOCKET NUMBER: P8074-7003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1889 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-861-747-3

Query Match 2.1%; Score 30; DB 3; Length 1889;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
Db 1843 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1872

RESULT 9

US-09-149-476-66
; Sequence 66, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626

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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
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EARLIER APPLICATION NUMBER: 60/056,881
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EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 2.1%: Score 29; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1368 TATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
Db 673 TATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 701

RESULT 10
US-09-615-192A-94
Sequence 94, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
MODIFICATION OF PLANT LIGNIN CONTENT
FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 94
LENGTH: 1012
TYPE: DNA
ORGANISM: Pinus radiata
US-09-615-192A-94

Query Match 2.1%: Score 29; DB 4; Length 1012;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1368 TATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
Db 984 TATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1012

RESULT 11
US-08-713-000-6
Sequence 6, Application US/08713000
Patent No. 5850020
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
APPLICANT: Grierson, Alastair
TITLE OF INVENTION: MATERIALS AND METHODS FOR THE
MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Speckman Picard PLLC
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,000
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-713-000-6

Query Match 2.1%: Score 29; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1368 TATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
Db 998 TATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1026

RESULT 12
US-08-975-316-6
Sequence 6, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N., Havukkala, Ilkka
APPLICANT: and Grierson, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185

```
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1003C1
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1026 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-975-316-6

Query Match      2.1%  Score 29; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1368 TATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
      |||||
DB 998 TATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1026

RESULT 13
US-09-211-710-6
; Sequence 6, Application US/09211710A
; Patent No. 6204434
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Grierson, Alastair
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c3
; CURRENT APPLICATION NUMBER: US/09/211,710A
; CURRENT FILING DATE: 1998-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Pinus radiata
; US-09-211-710-6

Query Match      2.1%  Score 29; DB 4; Length 1026;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1368 TATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
      |||||
DB 998 TATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1026

RESULT 14
US-09-615-192A-6
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; Sequence 6, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Pinus radiata
; US-09-615-192A-6

Query Match      2.1%  Score 29; DB 4; Length 1026;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1368 TATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
      |||||
DB 998 TATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1026

RESULT 15
US-08-605-106-3
; Sequence 3, Application US/08605106
; Patent No. 5910631
; GENERAL INFORMATION:
; APPLICANT: Topfer, R.
; APPLICANT: Martini, N.
; APPLICANT: Schell, J.
; TITLE OF INVENTION: MEDIUM CHAIN-SPECIFIC THIOESTERS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,106
; FILING DATE: 23-SEPT-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02935
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 235.001US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-373-6900
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1066 Base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: : c-DNA to m-RNA
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; ORGANISM: Cuphea lanceolata
; IMMEDIATE SOURCE:
; LIBRARY: c-DNA Bank ZAP
; CLONE: CITE12
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..875
; FEATURE:
; NAME/KEY: Stopcodon
; LOCATION: 876..878
US-08-605-106-3
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Query Match      2.1%; Score 29; DB 2; Length 1066;
Best Local Similarity 100.0%; Pred. NO. 0.0015;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1368 TATCAAAAAAAAAAAAAAAAAAAAAA 1396
      |||||
Db 1028 TATCAAAAAAAAAAAAAAAAAAAAAA 1056
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Search completed: February 2, 2003, 21:02:57
Job time : 93 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 21:01:29 : Search time 78 Seconds

(without alignments)
8040.688 Million cell updates/sec

Title: US-09-807-867-1

Perfect score: 1396

Sequence: 1 cgcctcacattggattcgt.....aaaaaaaaaaaaaaaaaaaa 1396

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OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 396772 seqs, 224632407 residues

Word size : 0

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	870	62.3	921	10	US-09-770-445-418
C 2	39	2.8	215	10	Sequence 418, App
C 3	31	2.2	1280	10	Sequence 66, Appl
C 4	31	2.2	1617	12	US-09-770-445-21
C 5	31	2.2	2243	10	Sequence 21, Appl
C 6	31	2.2	2485	10	Sequence 4, Appli
C 7	30	2.1	995	10	Sequence 43, Appl
C 8	30	2.1	1492	10	Sequence 451, App
C 9	30	2.1	2478	9	Sequence 244, App
C 10	30	2.1	2478	9	Sequence 112, App
C 11	30	2.1	2478	9	Sequence 176, App
C 12	30	2.1	2478	9	Sequence 476, App
C 13	30	2.1	2478	9	Sequence 476, App
C 14	30	2.1	2478	9	Sequence 107, App
C 15	30	2.1	2478	9	Sequence 107, App
C 16	30	2.1	2478	9	Sequence 107, App
C 17	30	2.1	2478	12	US-10-052-586-107
C 18	30	2.1	2493	9	Sequence 107, App
C 19	30	2.1	2645	10	Sequence 63, Appl
					Sequence 76, Appl

Sequence 9931, Ap
Sequence 544, App
Sequence 374, App
Sequence 351, App
Sequence 42, Appli
Sequence 237, App
Sequence 228, App
Sequence 32, Appli
Sequence 365, App
Sequence 276, App
Sequence 1247, Ap
Sequence 777, App
Sequence 2536, Ap
Sequence 2544, Ap
Sequence 3171, Ap
Sequence 13, Appl
Sequence 17, Appl
Sequence 4, Appli
Sequence 584, App
Sequence 584, App
Sequence 1063, Ap
Sequence 1063, Ap
Sequence 9541, Ap
Sequence 254, App

ALIGNMENTS

RESULT 1

US-09-770-445-418/c

; Sequence 418, Application US/09770445

; Patent No. US20020023281A1

; GENERAL INFORMATION:

; APPLICANT: Gorlach, Jorn

; APPLICANT: An, Yong-Qiang

; APPLICANT: Hamilton, Carol M.

; APPLICANT: Price, Jennifer L.

; APPLICANT: Raines, Tracy M.

; APPLICANT: Yu, Yang

; APPLICANT: Rameaka, Joshua G.

; APPLICANT: Page, Amy

; APPLICANT: Matthew, Abraham V.

; APPLICANT: Ledford, Brooke L.

; APPLICANT: Woessner, Jeffrey P.

; APPLICANT: Haas, William David

; APPLICANT: Garcia, Carlos A.

; APPLICANT: Krickler, Maja

; APPLICANT: Slader, Ted

; APPLICANT: Davis, Keith R.

; APPLICANT: Allen, Keith

; APPLICANT: Hoffman, Neil

; APPLICANT: Hurban, Patrick

; TITLE OF INVENTION: Expressed Sequences of Arabidopsis

; TITLE OF INVENTION: thaliana

; FILE REFERENCE: 2023US (PARA-012PRV)

; CURRENT APPLICATION NUMBER: US/09/770,445

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: US 60/178,472

; PRIOR FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 999

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 418

; LENGTH: 921

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-770-445-418

Query Match 62.3%; Score 870; DB 10; Length 921;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 920; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 CTCTTCAACTAGTGGCTTTTGGACATGATCATCAAGCTTGACGAAGAGTGAATGTTT 460
Db 921 CTCTTCAACTAGTGGCTTTTGGACATGATCATCAAGCTTGACGAAGAGTGAATGTTT 862
QY 461 TCCTTAGACAGACTGGTATTAAAGTACTTGGACACTTTGTATGTCGACCGAACAATGCAA 520
Db 861 TCCTTAGACAGACTGGTATTAAAGTACTTGGACACTTTGTATGTCGACCGAACAATGCAA 802
QY 521 GGTTCCTTGTCTTGGACAAATGCTAGAGTGCCTTATTTTGGTTTATGTCGTGCTAC 580
Db 801 GGTTCCTTGTCTTGGACAAATGCTAGAGTGCCTTATTTTGGTTTATGTCGTGCTAC 742
QY 581 ATATGATGAGACTTGGTGTGGAGGAGCAGATTTATTTGAAGTACACTTTTGTG 640
Db 741 ATATGATGAGACTTGGTGTGGAGGAGCAGATTTATTTGAAGTACACTTTTGTG 682
QY 641 AGAGCTGGAATGAATGCATCACTTCTCATATGAAAGAAATGGTGAAATCTTGTG 700
Db 681 AGAGCTGGAATGAATGCATCACTTCTCATATGAAAGAAATGGTGAAATCTTGTG 622
QY 701 GGTTCATGCTTTTCTGGCTCAGCAGATAGCAACCTTCTACTTCTATGACAGTGTCT 760
Db 621 GGTTCATGCTTTTCTGGCTCAGCAGATAGCAACCTTCTACTTCTATGACAGTGTCT 562
QY 761 TGATATCTTAAGCCCTAGAAATGAGATATCATCTTTTCGGAATGTGTGGAGAGTCATGCAT 820
Db 561 TGATATCTTAAGCCCTAGAAATGAGATATCATCTTTTCGGAATGTGTGGAGAGTCATGCAT 502
QY 821 ATCAGACTTATGATAAATTTCTCAAGCCAGTGGAGAGGAGTTGAAGATATGCTCGAC 880
Db 501 ATCAGACTTATGATAAATTTCTCAAGCCAGTGGAGAGGAGTTGAAGATATGCTCGAC 442
QY 881 CGGATATCGCAGTAAATATCTATCAGGAGGAGTCTTACTTACTTATGATGAGTTCCAAA 940
Db 441 CGGATATCGCAGTAAATATCTATCAGGAGGAGTCTTACTTACTTATGATGAGTTCCAAA 382
QY 941 CATCAGAAGTCCCAATATCTCAAGACCAAGTAAATAGAAAATCTATACGATGTGTTGTA 1000
Db 381 CATCAGAAGTCCCAATATCTCAAGACCAAGTAAATAGAAAATCTATACGATGTGTTGTA 322
QY 1001 ACATAGAGATGATGAAGCAGAACACTGCAACACATGAGAGCTTGTGAGACTCTAGCA 1060
Db 321 ACATAGAGATGATGAAGCAGAACACTGCAACACATGAGAGCTTGTGAGACTCTAGCA 262
QY 1061 GTCTGGTCTTCCACACTCCATTTTAGATGATGATGATGATGATGATGATGATGATGATG 1120
Db 261 GTCTGGTCTTCCACACTCCATTTTAGAAGATGATGATGATGATGATGATGATGATGATG 202
QY 1121 TTGTTCTCAGGAGGCTCATTCGGAAGGTATTTGTAGACTGCTCAAGAAATCCATTACAA 1180
Db 201 TTGTTCTCAGGAGGCTCATTCGGAAGGTATTTGTAGACTGCTCAAGAAATCCATTACAA 142
QY 1181 GTTAATAAATAGAAAGTAACTAAAGAAATTTATTTGTATGAGTCTATGAACATAGAT 1240
Db 141 GTTAATAAATAGAAAGTAACTAAAGAAATTTATTTGTATGAGTCTATGAACATAGAT 82
QY 1241 ATAATCCCATATCTTGGGAATTAAGGAATTAATGTGAATTTCCCATGCTTGTGCTAGTGT 1300
Db 81 ATAATCCCATATCTTGGGAATTAAGGAATTAATGTGAATTTCCCATGCTTGTGCTAGTGT 22
QY 1301 GTGAGAGATCAATACCCCTA 1321
Db 21 GTGAGAGATCAATACCCCTA 1

RESULT 2

US-09-770-696-66/c
; Sequence 66, Application US/09770696
; Patent No. US2001004490A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jorn
; APPLICANT: An, Yong-Qiang

; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Ted
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE OF INVENTION: thaliana
; FILE REFERENCE: 2031US (PARA-020PRV)
; CURRENT APPLICATION NUMBER: US/09/770,696
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 911
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 215
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-696-66

Query Match 2.8%; Score 39; DB 10; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 GACGGAGATGGCGCGATTTTCAGGCATCTCTCTGTGATC 161

Db 52 GACGGAGATGGCGCGATTTTCAGGCATCTCTCTGTGATC 14

RESULT 3

US-09-770-445-21/c

; Sequence 21, Application US/09770445

; Patent No. US2002023281A1

; GENERAL INFORMATION:

; APPLICANT: Goriach, Jorn

; APPLICANT: An, Yong-Qiang

; APPLICANT: Hamilton, Carol M.

; APPLICANT: Price, Jennifer L.

; APPLICANT: Raines, Tracy M.

; APPLICANT: Yu, Yang

; APPLICANT: Rameaka, Joshua G.

; APPLICANT: Page, Amy

; APPLICANT: Matthew, Abraham V.

; APPLICANT: Ledford, Brooke L.

; APPLICANT: Woessner, Jeffrey P.

; APPLICANT: Haas, William David

; APPLICANT: Garcia, Carlos A.

; APPLICANT: Kricker, Ted

; APPLICANT: Slader, Ted

; APPLICANT: Davis, Keith R.

; APPLICANT: Allen, Keith

; APPLICANT: Hoffman, Neil

; APPLICANT: Hurban, Patrick

; TITLE OF INVENTION: Expressed Sequences of Arabidopsis

; FILE OF INVENTION: thaliana

; FILE REFERENCE: 2023US (PARA-012PRV)

; CURRENT APPLICATION NUMBER: US/09/770,445

; PRIOR FILING DATE: 2001-01-26

; PRIOR FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 999

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1280
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1280)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-445-21

Query Match 2.2%; Score 31; DB 10; Length 1280;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1365 TTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1395
|||||
Db 31 TTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 4

US-10-093-045-4
; Sequence 4, Application US/10093045
; Patent No. US20020151708A1
; GENERAL INFORMATION:
; APPLICANT: Guerriero, Vincent
; APPLICANT: Raynes, Deborah A
; TITLE OF INVENTION: DNA Encoding Proteins That Inhibit Hsp70 Function
; FILE REFERENCE: HspBP DNA and Protein Sequences
; CURRENT APPLICATION NUMBER: US/10/093,045
; CURRENT FILING DATE: 2002-03-07
; EARLIER APPLICATION NUMBER: 09/444,336
; EARLIER FILING DATE: 1999-11-19
; EARLIER APPLICATION NUMBER: 60/109,351
; EARLIER FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-093-045-4

Query Match 2.2%; Score 31; DB 12; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1366 TTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
Db 1587 TTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1617

RESULT 5

US-09-764-864-43
; Sequence 43, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 2243
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-43

Query Match 2.2%; Score 31; DB 10; Length 2243;
Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1366 TTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
Db 2209 TTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 2239

RESULT 6

US-09-925-300-451
; Sequence 451, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 451
; LENGTH: 2485
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (222)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-451

Query Match 2.2%; Score 31; DB 10; Length 2485;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1366 TTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
Db 2438 TTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 2468

RESULT 7

US-09-770-445-244/c
; Sequence 244, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurlban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472

; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 244
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-244

Query Match 2.1%; Score 30; DB 10; Length 995;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
DB 52 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 8

US-09-925-299-112
; Sequence 112, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL02
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1487)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1491)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-112

Query Match 2.1%; Score 30; DB 10; Length 1492;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
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DB 1363 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1392

RESULT 9
US-09-978-295A-476
; Sequence 476, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 2.1%; Score 30; DB 9; Length 2478;
 Best Local Similarity 100.0%; Pred. No. 0.0045;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
 Db 2437 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2466

RESULT 10
 US-09-978-697-476
 ; Sequence 476, Application US/09978697
 ; Patent No. us20020169284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Bolstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.

APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
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PRIOR FILING DATE: 1998-05-06

PRIOR APPLICATION NUMBER: 60/084637
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 2.1% Score 30; DB 9; Length 2478;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
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DB 2437 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2466
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RESULT 11
US-09-978-192A-476
Sequence 476, Application US/09978192A
Patent No. US2002017553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084627
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084643
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/085339
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085338
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085582
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085700
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085689
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 2.1%; Score 30; DB 9; Length 2478;
 Best Local Similarity 100.0%; Pred. No. 0.0045;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
 Db 2437 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2466

RESULT 12

US-09-999-832A-476
 ; Sequence 476, Application US/09999832A
 ; Publication No. US20020192706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630PIC63

[illegible]

;< PRIOR APPLICATION NUMBER: 60/085339
;< PRIOR FILING DATE: 1998-05-13
;< PRIOR APPLICATION NUMBER: 60/085338
;< PRIOR FILING DATE: 1998-05-13
;< PRIOR APPLICATION NUMBER: 60/085323
;< PRIOR FILING DATE: 1998-05-13
;< PRIOR APPLICATION NUMBER: 60/085582
;< PRIOR FILING DATE: 1998-05-15
;< PRIOR APPLICATION NUMBER: 60/085700
;< PRIOR FILING DATE: 1998-05-15
;< PRIOR APPLICATION NUMBER: 60/085689
;< PRIOR FILING DATE: 1998-05-15
;< PRIOR APPLICATION NUMBER: 60/085579
;< PRIOR FILING DATE: 1998-05-15
;< PRIOR APPLICATION NUMBER: 60/085580
;< PRIOR FILING DATE: 1998-05-15
;< PRIOR APPLICATION NUMBER: 60/085573
;< PRIOR FILING DATE: 1998-05-15
;< PRIOR APPLICATION NUMBER: 60/085704
;< PRIOR FILING DATE: 1998-05-15
;< PRIOR APPLICATION NUMBER: 60/085697

Query Match 2.1%; Score 30; DB 9; Length 2478;

Best Local Similarity 100.0%; Pred.No. 0.0045;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAA 1396

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Db 2437 TTATCAAAAAAAAAAAAAAAAAAAAAAA 2466

RESULT 13

US-09-978-189-476

Sequence 476, Application US/09978189

Publication No. US20030004102A1

GENERAL INFORMATION:

;< APPLICANT: Ashkenazi, Avi
;< APPLICANT: Baker Kevin P.
;< APPLICANT: Botstein, David
;< APPLICANT: Desnoyers, Luc
;< APPLICANT: Eaton, Dan
;< APPLICANT: Fertara, Napoleon
;< APPLICANT: Filvaroff, Ellen
;< APPLICANT: Fong, Sherman
;< APPLICANT: Gao, Wei-Qiang
;< APPLICANT: Gerber, Hanspeter
;< APPLICANT: Gerlitsen, Mary E.
;< APPLICANT: Goddard, Audrey
;< APPLICANT: Godowski, Paul J.
;< APPLICANT: Grimaldi, J. Christopher
;< APPLICANT: Gurney, Austin L.
;< APPLICANT: Hillan, Kenneth J.
;< APPLICANT: Kljavin, Ivar J.
;< APPLICANT: Kuo, Sophia S.
;< APPLICANT: Napier, Mary A.
;< APPLICANT: Pan, James;
;< APPLICANT: Paonli, Nicholas F.
;< APPLICANT: Roy, Margaret Ann
;< APPLICANT: Shelton, David L.
;< APPLICANT: Stewart, Timothy A.
;< APPLICANT: Tumas, Daniel
;< APPLICANT: Williams, P. Mickey
;< APPLICANT: Wood, William I.
;< TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;< TITLE OF INVENTION: Acids Encoding the Same
;< FILE REFERENCE: P2630PIC7
;< CURRENT APPLICATION NUMBER: US/09/978,189
;< CURRENT FILING DATE: 2001-10-15
;< PRIOR APPLICATION NUMBER: 09/918585
;< PRIOR FILING DATE: 2001-07-30
;< PRIOR APPLICATION NUMBER: 60/062250
;< PRIOR FILING DATE: 1997-10-17
;< PRIOR APPLICATION NUMBER: 60/064249

; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
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; PRIOR APPLICATION NUMBER: 60/081838
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; PRIOR APPLICATION NUMBER: 60/082796
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; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
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; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 2.1%; Score 30; DB 9; Length 2478;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
Db 2437 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 2466
|||||

RESULT 14

US-10-174-590-107
; Sequence 107, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 107
; LENGTH: 2478
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-107

Query Match 2.1%; Score 30; DB 9; Length 2478;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
Db 2437 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 2466
|||||

RESULT 15

US-10-176-758-107
; Sequence 107, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 107
; LENGTH: 2478
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-758-107

Query Match 2.1%; Score 30; DB 9; Length 2478;
Best Local Similarity 100.0%; Pred. NO. 0.0045;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAA 1396
|||||
Db 2437 TTATCAAAAAAAAAAAAAAAAAAAAA 2466

Search completed: February 2, 2003, 22:44:41
Job time : 115 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 20:58:55 ; Search time 2242 Seconds
(without alignments)
10084.255 Million cell updates/sec

Title: US-09-807-867-1
Perfect score: 1396
Sequence: 1 ccgcacattgggttcgt.....aaaaaaaaaaaaaaaaaaaaa 1396

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST.*

1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_estl.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	39.8	574	10	AV829185
2	466	33.4	721	10	BE038851
3	449	32.2	630	10	AV440012
4	398	28.5	398	10	AV536756
5	394	28.2	579	9	A1997645
6	282	20.2	432	10	AV798458

c	7	277	19.8	413	10	AV814996
c	8	268	19.2	472	9	A1994896
c	9	253	18.1	253	10	AV562439
c	10	235	16.8	422	10	AV808193
c	11	232	16.6	261	10	BE527658
c	12	218	15.6	284	10	BE522866
c	13	173	12.4	173	10	AV441747
c	14	131	9.4	376	10	AV804850
c	15	130	9.3	1166	17	B09762
c	16	93	6.7	520	10	AV544091
c	17	91	6.5	426	14	T42793
c	18	88	6.3	171	10	AV552557
c	19	84	6.0	415	9	AA395166
c	20	63	4.5	267	14	R30022
c	21	48	3.4	670	17	BH563128
c	22	37	2.7	300	12	BG511663
c	23	35	2.5	276	10	BE057322
c	24	35	2.5	353	9	AI074729
c	25	34	2.4	222	13	BM565902
c	26	34	2.4	238	13	BM566385
c	27	33	2.4	275	12	BF777697
c	28	33	2.4	357	10	AW415996
c	29	33	2.4	394	10	BE668854
c	30	33	2.4	399	10	AV806414
c	31	33	2.4	470	13	BI945764
c	32	33	2.4	483	13	BM396187
c	33	33	2.4	510	10	BE030519
c	34	33	2.4	601	14	BQ522145
c	35	33	2.4	670	14	BQ412053
c	36	33	2.4	752	12	BG440527
c	37	33	2.4	864	12	BG167921
c	38	33	2.4	1739	11	AV104099
c	39	32	2.3	68	9	AJ281323
c	40	32	2.3	82	9	A1540303
c	41	32	2.3	124	14	BQ792800
c	42	32	2.3	168	13	BI945315
c	43	32	2.3	172	13	BI316657
c	44	32	2.3	173	14	BQ799719
c	45	32	2.3	191	12	BG893813

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
AV829185 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-40-M04 5', mRNA linear EST 01-APR-2002
mRNA sequence.
ACCESSION
AV829185
VERSION
AV829185.1
KEYWORDS
EST, GI:19871245
SOURCE
Arabidopsis thaliana
ORGANISM
thale cress.
REFERENCE
1 (bases 1 to 574)
AUTHORS
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
TITLE
Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL
Unpublished (2002)
COMMENT
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI

AV814996	AV814996
A1994896	701500351
AV562439	AV562439
AV808193	AV808193
BE527658	M69K21STM
BE522866	M29G11STM
AV441747	AV441747
AV804850	AV804850
B09762	P24K2-Sp6 I
AV544091	AV544091
T42793	6056 Lambda
AV552557	AV552557
AA395166	26963 Lam
R30022	12627 Lambd
BM563128	BOGLG18TF
BG511663	sa090807
BE057322	sn01e09.Y
AI074729	ox83g04.s
BM565902	rt04f04.Y
BM566385	rt04f04.Y
BF777697	NXSI_073
AW415996	50650 MAR
BE668854	159239 MA
AV806414	AV806414
BI945764	sc68g02.Y
BM396187	5009-0-18
BE030519	128620 MA
BQ522145	N1SC_n115
BQ412053	GA_EG005
BG440527	GA_EG000
BG167921	602340006
AV104099	zea mays
AJ281323	4A3A-P2A1
A1540303	tc34006.x
BQ792800	EST 7705
BI945315	sb55d03.Y
BI316657	sa71c01
BQ799719	EST 1888
BG893813	kt15g01.Y

4

Qy	458	TTTTCCTTACAGAC	CTCGGTTAATTAAGATACATTGACACTTTGTATCGTGACCGAACATATG	517		
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Qy	518	CAAGGTTCTTTGTTCTT	CGAGACAAATGCTACAGTGCCTTAATTTTTCGCTTTATGTCGTGTC	577		
Db	120	CAAGGTTCTTTGTTCTT	CGAGACAAATGCTACAGTGCCTTAATTTTTCGCTTTATGTCGTGTC	179		
Qy	578	TACATATGATGAGAC	CTTTGGTGGAGGAGCAGCATATTTTGAAGTACACATTTG	637		
Db	180	TACATATGATGAGAC	CTTTGGTGGAGGAGCAGCATATTTTGAAGTACACATTTG	239		
Qy	638	CTGAGAGCTGGAATGA	AGATGCATGCATGCTCATATGAATGGAAGAAATGGGTGGAAATTC	697		
Db	240	CTGAGAGCTGGAATGA	AGATGCATGCATGCTCATATGAATGGAAGAAATGGGTGGAAATTC	299		
Qy	698	GGTGGTTTGATCG	TTTTTCTGGCTCAGCA	725		
Db	300	GGTGGTTTGATCG	TTTTTCTGGCTCAGCA	327		
RESULT 9						
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LOCUS		AV562439	Arabidopsis thaliana green siliques Columbia	EST 07-SEP-2000		
DEFINITION		thaliana cDNA clone SQ170b03F 3', mRNA sequence.				
ACCESSION		AV562439				
VERSION		AV562439.1	GI:8733865			
KEYWORDS		EST.				
SOURCE		thale cress.				
ORGANISM		Arabidopsis thaliana				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.					
	1 (bases 1 to 253)					
	Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.					
	A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries					
	DNA Res. 7, 175-180 (2000)					
JOURNAL	20363093					
MEDLINE						
COMMENT	Contact: Erika Asamizu The First Laboratory For Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.					
FEATURES	source					
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	/organism="Arabidopsis thaliana"					
	/strain="Columbia"					
	/db_xref="taxon:3702"					
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	Best Local Similarity 100.0%; Pred. No. 3.2e-52;					
	Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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Qy	1159	TGCGTCAAGAAATCCAT	TACAGTTAATAATTAGAAGTAACTAAAAAGATTATTG	1218		
Db	193	TGCGTCAAGAAATCCAT	TACAGTTAATAATTAGAAGTAACTAAAAAGATTATTG	134		
Qy	1219	TATCAGCTCATGAACA	TAGATATAATCCCATATACTTGGGAATPAAGGAATAATGTCAA	1278		

Db 244 TCTCCACACTCCATTTTAGAAGATGATGATCTGAACAAGATCAGGGTGTGTTTTCTCT 185
 QY 1129 GAGGAGCTCAATCGGAGGATTTGTAGACTGCTCAAGAAATCCATTACAAGTTAATAA 1188
 Db 184 GAGGAGCTCAATCGGAGGATTTGTAGACTGCTCAAGAAATCCATTACAAGTTAATAA 125
 QY 1189 ATTAGAAGTAACTAAAAAGATTATTTGTATCAGCTCATGAACAATAGATATAATCCC 1248
 Db 124 ATTAGAAGTAACTAAAAAGATTATTTGTATCAGCTCATGAACAATAGATATAATCCC 65
 QY 1249 ATATAGTGGGAATAAAGGAATAATGTGAATCCCA 1285
 Db 64 ATATAGTGGGAATAAAGGAATAATGTGAATCCCA 28

RESULT 11
 BE527658 261 bp mRNA linear EST 19-MAR-2001
 LOCUS M69K21STM Arabidopsis developing seed Arabidopsis thaliana cDNA
 DEFINITION clone 600036586R1 5', mRNA sequence.

ACCESSION BE527658
 VERSION BE527658.1 GI:9785636
 KEYWORDS EST.
 SOURCE thale cress.

ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 261)
 AUTHORS White,J.A., Todd,J., Newman,T., Focke,N., Girke,T., Martinez de
 Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C.
 TITLE A new set of Arabidopsis expressed sequence tags from developing
 seeds. The metabolic pathway from carbohydrates to seed oil
 JOURNAL Plant Physiol. 124 (4), 1582-1594 (2000)
 MEDLINE 20567808
 COMMENT Contact: Benning, C
 Dept. of Biochemistry & Molecular Biology
 Michigan State University
 224 Biochemistry, Michigan State University, East Lansing, MI 48824
 , USA
 Tel: 517 355 1609
 Fax: 517 353 9334
 Email: benning@msu.edu

Clones were originally prepared at Michigan State University.
 Arabidopsis Biological Resource Center, The Ohio State University,
 309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210
 USA, FAX: 6142920603 TEL: 6142929371.
 FEATURES
 source
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 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="600036586R1"
 /clone_lib="Arabidopsis developing seed"
 /tissue_type="seed"
 /dev_stage="5-13 days after flowering"
 /lab_host="E.coli"
 /note="Organ: Developing seed; Vector: pBluescript SK-;
 Site_1: EcoRI; Site_2: XhoII"
 BASE COUNT 56 a 68 c 52 g 85 t

Query Match 16.6%; Score 232; DB 10; Length 261;
 Best Local Similarity 100.0%; Pred. No. 3.8e-47;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGCTCACATTTGGGATTCGTCATTTCTTCTAAACCCGCAAAATTTCTCCATTTCTAC 60
 Db 30 CCGCTCACATTTGGGATTCGTCATTTCTTCTAAACCCGCAAAATTTCTCCATTTCTAC 89
 QY 61 CAAAAATATCAACTTTTACTTTTCTTCTGTGAAATTTATCTGCTCAAAATCTTTGGTTC 120

Db 124 ATTAGAAGTAACTAAAAAGATTATTTGTATCAGCTCATGAACAATAGATATAATCCC 65
 QY 1129 GAGGAGCTCAATCGGAGGATTTGTAGACTGCTCAAGAAATCCATTACAAGTTAATAA 1188
 Db 184 GAGGAGCTCAATCGGAGGATTTGTAGACTGCTCAAGAAATCCATTACAAGTTAATAA 125
 QY 1189 ATTAGAAGTAACTAAAAAGATTATTTGTATCAGCTCATGAACAATAGATATAATCCC 1248
 Db 124 ATTAGAAGTAACTAAAAAGATTATTTGTATCAGCTCATGAACAATAGATATAATCCC 65
 QY 1249 ATATAGTGGGAATAAAGGAATAATGTGAATCCCA 1285
 Db 64 ATATAGTGGGAATAAAGGAATAATGTGAATCCCA 28

Db 90 CAAAAATATCAACTTTTACTTTTCTTCTGTGAAATTTATCTGCTCAAAATCTTTGGTTC 149
 QY 121 CTGACGGAGATGGCGGATTTTCAGGCATCTCTCTGTGTACGTTGACGATTTTCACGGGCT 180
 Db 150 CTGACGGAGATGGCGGATTTTCAGGCATCTCTCTGTGTACGTTGACGATTTTCACGGGCT 209
 QY 181 TTGGTTACTCTTCGAGCGCTCTAGAGCGCGGTTTTCGTACAGCTCTCTCTCACC 232
 Db 210 TTGGTTACTCTTCGAGCGCTCTAGAGCGCGGTTTTCGTACAGCTCTCTCTCACC 261

RESULT 12
 BE522866 284 bp mRNA linear EST 19-MAR-2001
 LOCUS M29G11STM Arabidopsis developing seed Arabidopsis thaliana cDNA
 DEFINITION clone M29G11 5', mRNA sequence.

ACCESSION BE522866
 VERSION BE522866.1 GI:9780844
 KEYWORDS EST.
 SOURCE thale cress.

ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 284)
 AUTHORS White,J.A., Todd,J., Newman,T., Focke,N., Girke,T., Martinez de
 Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C.
 TITLE A new set of Arabidopsis expressed sequence tags from developing
 seeds. The metabolic pathway from carbohydrates to seed oil
 JOURNAL Plant Physiol. 124 (4), 1582-1594 (2000)
 MEDLINE 20567808
 COMMENT Contact: Benning, C
 Dept. of Biochemistry & Molecular Biology
 Michigan State University
 224 Biochemistry, Michigan State University, East Lansing, MI 48824
 , USA
 Tel: 517 355 1609
 Fax: 517 353 9334
 Email: benning@msu.edu

Clones were originally prepared at Michigan State University.
 Arabidopsis Biological Resource Center, The Ohio State University,
 309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210
 USA, FAX: 6142920603 TEL: 6142929371.
 FEATURES
 source
 1. .284
 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="M29G11"
 /clone_lib="Arabidopsis developing seed"
 /tissue_type="seed"
 /dev_stage="5-13 days after flowering"
 /lab_host="E.coli"
 /note="Organ: Developing seed; Vector: pBluescript SK-;
 Site_1: EcoRI; Site_2: XhoII"
 BASE COUNT 55 a 83 c 49 g 96 t 1 others

Query Match 15.6%; Score 218; DB 10; Length 284;
 Best Local Similarity 99.6%; Pred. No. 8.7e-44;
 Matches 268; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCGCTCACATTTGGGATTCGTCATTTCTTCTTAAACCCGCAAAATTTCTCCATTTCTAC 60
 Db 16 CCGCTCACATTTGGGATTCGTCATTTCTTCTTAAACCCGCAAAATTTCTCCATTTCTAC 75
 QY 61 CAAAAATATCAACTTTTACTTTTCTTCTGTGAAATTTATCTGCTCAAAATCTTTGGTTC 120
 Db 76 CAAAAATATCAACTTTTACTTTTCTTCTGTGAAATTTATCTGCTCAAAATCTTTGGTTC 135
 QY 121 CTGACGGAGATGGCGGATTTTCAGGCATCTCTCTGTGTACGTTGACGATTTTCACGGGCT 180
 Db 136 CTGACGGAGATGGCGGATTTTCAGGCATCTCTCTGTGTACGTTGACGATTTTCACGGGCT 195

QY 181 TTGGTTACTCTTCGAGCGCTAGAGCCGCTTCGTACAGCTCCTCTCACCATTGCTT 240
|||||
Db 196 TTGGTTACTCTTCGAGCGCTAGAGCCGCTTCGTACAGCTCCTCTCACCATTGCTT 255
|||||

QY 241 CATCATCTTCCTCTCTCTTCGTCGTCT 269
|||||
Db 256 CATCATCTTCCTCTCTCTTCGTCGTCT 284
|||||

RESULT 13
AV441747
LOCUS
DEFINITION AV441747 Arabidopsis thaliana above-ground organ two to six-week
old Arabidopsis thaliana cDNA clone APD34b10_r 5', mRNA sequence.
ACCESSION AV441747
VERSION AV441747.1 GI:7612140
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
source
1..173
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="APD34b10_r"
/clone_lib="Arabidopsis thaliana above-ground organ two to
six-week old"
/tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 40 a 44 c 27 g 62 t
ORIGIN
Query Match 12.4%; Score 173; DB 10; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTCACATGGGATTCGTCATCTCTCTTCTAAACCCGCAAAATTCCTCAATTTCTACCA 63
|||||
Db 1 CTCACATGGGATTCGTCATCTCTCTTCTAAACCCGCAAAATTCCTCAATTTCTACCA 60
|||||

QY 64 AAATATCCAACCTTTTACTTTTCTTCGTCGTAATATATCTGCTCAAAATCTTTGGTTCTG 123
|||||
Db 61 AAATATCCAACCTTTTACTTTTCTTTCTTCGTCGTAATATATCTGCTCAAAATCTTTGGTTCTG 120
|||||

QY 124 ACGGAGATGGCGGATTTTCAGGCATCTCCCTCTGTCGTAGCTTGACGATTTTCACG 176
|||||
Db 121 ACGGAGATGGCGGATTTTCAGGCATCTCCCTCTGTCGTAGCTTGACGATTTTCACG 173
|||||

RESULT 14
AV804850/c
LOCUS
DEFINITION AV804850 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-40-M04 3',
mRNA sequence.
ACCESSION AV804850

AV804850.1 GI:19838835
EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msekierc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.

FEATURES
source
1..376
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAFL09-40-M04"
/clone_lib="RAFL9"
/dev_stage="plants at various developmental stages from
germination to mature seeds"
/lab_host="DH10B"
/note="Site_1: BamHI; Site_2: SalI; subjected to
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
hr) treatments"

BASE COUNT 104 a 77 c 59 g 136 t
ORIGIN
Query Match 9.4%; Score 131; DB 10; Length 376;
Best Local Similarity 99.5%; Pred. No. 8.2e-23;
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 966 ACCAGTAATAGAAAATCTATACGATGTGTTGTGAACATAAGAGATGATGAAGCAACA 1025
|||||
Db 376 ACCAGTAATAGAAAATCTATACGATGTGTTGTGAACATAAGAGATGATGAAGCAACA 317
|||||

QY 1026 CTCGAAGACAATGAGAGCTGTGCAGACTCTAGCGACTGCGTCTCCACACTCCATTTT 1085
|||||
Db 316 CTCGAAGACAATGAGAGCTGTGCAGACTCTAGCGACTGCGTCTCCACACTCCATTTT 257
|||||

QY 1086 AGATGATGATGATCTGAAGAAGAAATCAGGGTGTGTTGTTCTCTGAGGAGGCTCATTTGCGA 1145
|||||
Db 256 AGAAGATGATGATCTGAAGAAGAAATCAGGGTGTGTTGTTCTCTGAGGAGGCTCATTTGCGA 197
|||||

QY 1146 AG 1147
||
Db 196 AG 195

RESULT 15
B09762
LOCUS
DEFINITION B09762 IGF Arabidopsis thaliana genomic clone F24K2, DNA
sequence.
ACCESSION B09762
VERSION B09762.1 GI:2090881
KEYWORDS GSS.
SOURCE thale cress.

ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 1166)
 REFERENCE Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and
 AUTHORS Ecker, J.
 TITLE BAC End Sequences at ATGC
 JOURNAL Unpublished (1997)
 COMMENT Other GSSS: F24K2-T7
 Contact: Ecker J.
 Arabidopsis Thaliana Genome Center
 University of Pennsylvania
 Dept. of Biology, University of Pennsylvania, Philadelphia, PA
 19104
 Tel: 215-898-9384
 Fax: 215-898-8780
 Email: jecker@atgenome.bio.upenn.edu
 Seq primer: Sp6
 Class: BAC ends
 High quality sequence start: 50
 High quality sequence stop: 865.
 FEATURES
 source
 1..1166
 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="F24K2"
 /clone_lib="IGF"
 /sex="hermaphrodite"
 /note="Vector: BelobACII; Site_1: EcoRI; Site_2: EcoRI;
 Produced by Thomas Altmann"

BASE COUNT 315 a 232 c 218 g 399 t 2 others
 ORIGIN
 Query Match 9.3%; Score 130; DB 17; Length 1166;
 Best Local Similarity 100.0%; Pred. No. 5.1e-23;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGCTCACATTGGGATTCGTCATTTCTTTCTTAAACCCGCAAAATTTCTCCATTCTTAC 60
 Db 475 |||||
 QY 61 CAAAATATCCAACTTTTACTTTTCTTTCCCTGTGAATTTATCTGCTCAAAATCTTTGGTTTC 120
 Db 535 |||||
 QY 121 CTGACGGAGA 130
 Db 595 CTGACGGAGA 604

Search completed: February 2, 2003, 22:42:54
 Job time : 2265 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2003, 21:03:06 ; Search time 70 seconds
(without alignments)
668.157 Million cell updates/sec

Title: US-09-807-867-2

Perfect score: 1845

Sequence: 1 MAATSGISSGTLTISRPLVT.....VPEAHCEGIVDCLKRSITS 351

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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- 2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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- 15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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- 20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1845	100.0	351	21	Terminal oxidase a
2	1739	94.3	335	23	Herbicidally activ
3	196.5	10.7	318	21	Arabidopsis thalia
4	194.5	10.5	282	23	Herbicidally activ
5	192	10.4	587	21	Arabidopsis thalia
6	192	10.4	593	21	Arabidopsis thalia
7	192	10.4	595	21	Arabidopsis thalia
8	191.5	10.4	347	21	An alternative oxi
9	187.5	10.2	242	21	Arabidopsis thalia
10	187.5	10.2	282	21	Arabidopsis thalia

11	187.5	10.2	329	21	AAG48768	Arabidopsis thalia
12	187.5	10.2	329	23	ABB92457	Herbicidally activ
13	187	10.1	287	23	ABB91225	Herbicidally activ
14	185.5	10.1	353	21	AAG49606	Arabidopsis thalia
15	185.5	10.1	354	21	AAG49605	Arabidopsis thalia
16	185.5	10.1	354	23	ABB92395	Herbicidally activ
17	185.5	10.1	386	21	AAG49604	Arabidopsis thalia
18	184	10.0	329	21	AAB08002	An alternative oxi
19	178.5	9.7	175	21	AAG22099	Arabidopsis thalia
20	178.5	9.7	179	21	AAG22098	Arabidopsis thalia
21	177	9.6	401	23	ABB76399	Phaffia rhodozyma
22	176.5	9.6	323	21	AAG49603	Arabidopsis thalia
23	176.5	9.6	324	21	AAG49602	Arabidopsis thalia
24	176.5	9.6	325	21	AAG49601	Arabidopsis thalia
25	176.5	9.6	325	23	ABB92394	Herbicidally activ
26	169.5	9.2	174	21	AAG44170	Arabidopsis thalia
27	169.5	9.2	175	21	AAG44169	Arabidopsis thalia
28	153.5	8.3	357	23	AAM50305	Pichia stipitis SH
29	151	8.2	164	21	AAG44171	Arabidopsis thalia
30	101.5	5.5	461	23	ABP27470	Streptococcus poly
31	100	5.4	444	21	AAB41810	Human OREF ORF1574
32	100	5.4	444	21	AA97539	Human fatty acid d
33	100	5.4	444	21	AA59182	Human oxidoreducta
34	100	5.4	444	22	AAE11083	Human delta-6-Desa
35	100	5.4	444	22	AAM93425	Human polypeptide,
36	100	5.4	473	22	AAE11084	C-terminal tagged
37	96	5.2	917	22	AU34107	Staphylococcus aur
38	96	5.2	920	22	AU36588	Staphylococcus aur
39	96	5.2	920	22	AU37402	Staphylococcus aur
40	96	5.2	920	22	AU37555	Staphylococcus aur
41	95	5.1	1252	22	ABB66357	Drosophila melanog
42	93.5	5.1	699	22	ABB59209	Drosophila melanog
43	91.5	5.0	600	22	ABB58933	Drosophila melanog
44	90.5	4.9	312	21	AAG08413	Arabidopsis thalia
45	90	4.9	1418	22	ABG02184	Novel human diagno

ALIGNMENTS

RESULT 1

AA984869

ID AA984869 standard; Protein: 351 AA.

XX AA984869;

AC AA984869;

DT 08-AUG-2000 (first entry)

XX Terminal oxidase associated with biosynthesis of carotenoids.

DE Terminal oxidase; carotenoid biosynthesis; OTBC; phytoene desaturase;

KW carotenoid production; fruit colour; tomato; variegated leave;

KW Vitamin A precursor; beta-carotene; high light intensity; plant injury.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

PH Key Location/Qualifiers

FT Peptide 1..57

FT Cleavage-site 56..57 /note= "chloroplast transit signal peptide"

XX FR2784688-A1.

XX 21-APR-2000.

XX 20-OCT-1998; 98FR-0013283.

XX 20-OCT-1998; 98FR-0013283.

XX (UYGR-) UNIV GRENoble FOURIER JOSEPH.

XX Carol S, Kuntz M, Mache R, Coupland G, Stevenson D;

DR WPI; 2000-331435/29.
XX N-PSDB; AAA14951.
PT New DNA encoding terminal oxidase associated with biosynthesis of
PT carotenoids, useful for altering carotenoid content of plants, e.g.
PT changing fruit color -
XX
PS Claim 5; Fig 1; 34pp; French.
XX
CC The present sequence represents a protein that is a terminal oxidase
CC associated with biosynthesis of carotenoids (ORBC). The polypeptide
CC is associated with carotenoid biosynthesis. The enzyme is found in
CC chloroplast membranes, and is necessary for the function of phytoene
CC desaturase. The ORBC polynucleotide is used to increase carotenoid
CC production in plants, while its complement is used for antisense
CC inhibition of carotenoid biosynthesis, e.g. for modifying the color
CC of fruits such as tomatoes; to generate plants with variegated leaves
CC and to increase the content of the Vitamin A precursor beta-carotene
CC (which is also an anti-oxidant and colorant). Beta-Carotenoids also
CC protect plants against injury caused by high light intensity.
XX
SQ Sequence 351 AA;
Query Match 100.0%; Score 1845; DB 21; Length 351;
Best Local Similarity 100.0%; Pred. No. 9.9e-203;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAISGSGTLTISRPLVTLRRSRAAVSYSSSHRLLHLLPLSSRLLLRNNHRVQATIL 60
Db 1 MAAISGSGTLTISRPLVTLRRSRAAVSYSSSHRLLHLLPLSSRLLLRNNHRVQATIL 60
QY 61 QDDEKVVVEESFKAETSTGTETPLEEPNMSSTSAFETWIIKLEQGVNVLTDVSIKIL 120
Db 61 QDDEKVVVEESFKAETSTGTETPLEEPNMSSTSAFETWIIKLEQGVNVLTDVSIKIL 120
QY 121 DTLYRDRTYARFFVLETIARVPYFAPMSVLHMYETFGWRRADYLVKVFPAESWNEHHLL 180
Db 121 DTLYRDRTYARFFVLETIARVPYFAPMSVLHMYETFGWRRADYLVKVFPAESWNEHHLL 180
QY 181 IMEELGNSWDFRFLAQHIAIFYFYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLKA 240
Db 181 IMEELGNSWDFRFLAQHIAIFYFYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLKA 240
QY 241 SGEELKNMPADIAVXYTGGDLYLDFEQTSTRTPNTRRPVNIENLYDVFNIRDDAEHC 300
Db 241 SGEELKNMPADIAVXYTGGDLYLDFEQTSTRTPNTRRPVNIENLYDVFNIRDDAEHC 300
QY 301 KTRACOTLGLSRSPHSIILDDDDTEESGCVVPEEAHCEGIVDCLKKSITS 351
Db 301 KTRACOTLGLSRSPHSIILDDDDTEESGCVVPEEAHCEGIVDCLKKSITS 351
RESULT 2
AB93048
ID AB93048 standard; Protein: 335 AA.
XX
AC AB93048;
XX
DT 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 2259.
XX
KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP09892.
XX
PR 28-AUG-2001; 2001WO-EP09892.

XX (FARB) BAYER AG.
XX
XX Tietjen K, Weidler M;
XX WPI; 2002-269010/31.
DR
XX
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms -
XX
PS Claim 5; SEQ ID NO 2259; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins
CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
CC aligning and comparing nucleic acid or amino acid sequences from plant
CC with nucleic acid or amino acid sequences from non-plant organisms using
CC suitable search parameters, where plant sequences having an E-value
CC greater by a factor of 3 than the E-value of most similar non-plant
CC sequences are selected. The polypeptides or nucleic acids encoding them
CC are useful for identifying modulators. The identified modulators are
CC useful as herbicides.
XX
SQ Sequence 335 AA;
Query Match 94.3%; Score 1739; DB 23; Length 335;
Best Local Similarity 95.2%; Pred. No. 1.4e-190;
Matches 334; Conservative 1; Mismatches 0; Indels 16; Gaps 1;
QY 1 MAATGSSGTLTISRPLVTLRRSRAAVSYSSSHRLLHLLPLSSRLLLRNNHRVQATIL 60
Db 1 MAATGSSGTLTISRPLVTLRRSRAAVSYSSSHRLLHLLPLSSRLLLRNNHRVQATIL 60
QY 61 QDDEKVVVEESFKAETSTGTETPLEEPNMSSTSAFETWIIKLEQGVNVLTDVSIKIL 120
Db 61 QDDEKVVVEESFKAETSTGTETPLEEPNMSSTSAFETWIIKLEQGVNVLTDVSIKIL 120
QY 121 DTLYRDRTYARFFVLETIARVPYFAPMSVLHMYETFGWRRADYLVKVFPAESWNEHHLL 180
Db 121 DTLYRDRTYARFFVLETIARVPYFAPMSVLHMYETFGWRRADYLVKVFPAESWNEHHLL 180
QY 181 IMEELGNSWDFRFLAQHIAIFYFYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLKA 240
Db 181 IMEELGNSWDFRFLAQHIAIFYFYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLKA 240
QY 241 SGEELKNMPADIAVXYTGGDLYLDFEQTSTRTPNTRRPVNIENLYDVFNIRDDAEHC 300
Db 241 SGEELKNMPADIAVXYTGGDLYLDFEQTSTRTPNTRRPVNIENLYDVFNIRDDAEHC 284
QY 301 KTRACOTLGLSRSPHSIILDDDDTEESGCVVPEEAHCEGIVDCLKKSITS 351
Db 285 KTRACOTLGLSRSPHSIILDDDDTEESGCVVPEEAHCEGIVDCLKKSITS 335
RESULT 3
AAG22097
ID AAG22097 standard; Protein: 318 AA.
XX
AC AAG22097;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24896.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX

PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
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QY 185 LGGNSWDFRELAQHIAITFYFMTVLYILSPRMAYHFSECVESHAYETYDKFLK-ASGE 243
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Db 225 V-ARKPKWTERALVLAVQGVFFNAVFLGVLISPKFAHRVVGYLEBEAHTSVTEYKDLKLEAG 283
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QY 244 ELKNWPADPIAVKYTGDDLYLDFEFQTSRTPNTRRPVNIENLYDVFNIRDEAEH 299
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 284 KIENPAPAIAIDYW-----QLPADATLKDQVVVVVRSDEAHH 320
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RESULT 9
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XX
AC AAG48770;
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XX 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 61622.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 28-OCT-1999; 99US-0161992.


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SQ Query Match 10.2%; Score 187.5; DB 23; Length 329;
Best Local Similarity 25.5%; Pred. No. 2.2e-12;
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Db 107 EYKADL---TIDLKHHVPSTLPDKIAYWVK-----SLRPTDLFFQRRYGC 152
Qy 131 RFVLETIARVPYFAPMSVLHM-----YETFGWRRADYLVKVFHFAESNEMHLLIMEEL 185
Db 153 RAIMLETVAAPVGMVGMMLHFKLSRRFEQSGW-----IKALLEEAENRMLMTMEV 207
Qy 186 GNSWDFRFLAQHATATYFMTVFLYILSPRMAYHFSECVESHAYETDYKFLK-ASGEE 244
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Qy 245 LKNMPADIAVKYTYTGGDLYLDFDEFOTSRTPNTRRPVNIENLYDVFVNIRDEAEH 299
Db 267 IENVPAIAVDYW-----RLEADATLRDVMVVRDEAAH 302

RESULT 13
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ID ABB91225 standard; Protein; 287 AA.
XX
AC ABB91225;
XX
DT 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 436.
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KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP09892.
PR 28-AUG-2001; 2001WO-EP09892.
PA (FARB ) BAYER AG.
XX
PI Tietjen K, Weidner M;
XX
DR WPI; 2002-269010/31.
XX
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms -
XX
PS Claim 5; SEQ ID NO 436; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins
CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
CC aligning and comparing nucleic acid or amino acid sequences from plant
CC with nucleic acid or amino acid sequences from non-plant organisms using
CC suitable search parameters, where plant sequences having an E-value
CC greater by a factor of 3 than the E-value of most similar non-plant
CC sequences are selected. The polypeptides or nucleic acids encoding them
CC are useful for identifying modulators. The identified modulators are
CC useful as herbicides.
XX
SQ Sequence 287 AA;
Query Match 10.1%; Score 187; DB 23; Length 287;
Best Local Similarity 26.2%; Pred. No. 2.1e-12;

Matches 80; Conservative 47; Mismatches 102; Indels 76; Gaps 17;

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Db 11 RPLVSSVQSSGLGIGGRGH-LISHLP--NVRLLSSDTSPPVSGNNOENPIRTAD-CK 66
Qy 67 VVVEESFKAETSTGTPE--LEEPNMSSTSAFETWIKLEQGVNVLDTSVIKILDTLY 124
Db 67 VI-----STYWGIPPTKTKPDGSAWKNCQPW-----DSYKPDVSI----- 104
Qy 125 RDRTY-ARFVLETIARVPYFAPMSVLHM-----YETFGWRRADYLVKVFHFAESNEMHH 178
Db 105 -DRKHMCHAMLETVAAPVGMVGMMLHFKLSRRFEHSGGW-----IKALLEEAENRMH 158
Qy 179 LLIMEELGGNSWDFR--FLAQHATATYFMTVFLYILSPRMAYHFSECVESHAYETDY 235
Db 159 LMTFIEL-SQPKWYERALVISOGVFFNAYLIGYIISPKLAHRTGYLEEEAVNSYT 214
Qy 236 KFLK-ASGEELKNMPADIAVKYTYTGGDLYLDFDEFOTSRTPNTRRPVNIENLYDVFVNIR 294
Db 215 EFLKIDIDAGKFENSPAPAIADYW-----RLEADATLRDVMVVRDEAAH 302
Qy 295 DEAEH 299
Db 256 DEAHH 260

RESULT 14
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ID AAG49606 standard; Protein; 353 AA.
XX
AC AAG49606;
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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62771.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPL033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
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PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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## SUMMARIES

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## ALIGNMENTS

## RESULT 1

RESOL I  
US-09-556-601-26

03 03 336 001 20  
; Sequence 26, Application US/095556601

; Patent No. 6391599

; GENERAL INFORMATION:

APPLICANT: Jefferies, Thomas W.

APPLICANT: Shi, Nian Qing

; TITLE OF INVENTION: SHAM-SENSITIVE TERMINAL OXIDASE GENE FROM

; TITLE OF INVENTION: XYLOSE-FERMENTING YEAST

; FILE REFERENCE: 96429.9074

; CURRENT APPLICATION NUMBER: US/09/556,601

; CURRENT FILING DATE: 2000-04-21

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: Word 97 (DOS text format)

; SEQ ID NO 26

; LENGTH: 357

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; TYPE: PRT

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; ORGANISM: Pichia stipitis

US-09-556-601-26

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Best Local Similarity 22.8%; Pred No 3 5e-09.

BEST LOCAL SIMILARITY 22.88; Pred. No. 3.5e-09;  
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| Sequence 560, App  |
| Sequence 405, App  |

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## RESULT 2

US-08-220-151-5

; Sequence 5, Application US/08220151

; Patent No. 5529780

; GENERAL INFORMATION:

; APPLICANT: Paoletti, Enzo

; APPLICANT: Limbach, Keith J.

; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF

; TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C AND 9D AND USES THEREFOR

; NUMBER OF SEQUENCES: 91

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Curtis, Morris &amp; Safford

; STREET: 530 Fifth Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/220,151

; FILING DATE: 30-MAR-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Frommer, William S.

; REGISTRATION NUMBER: 25,506

; REFERENCE/DOCKET NUMBER: 454310-2540

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 840-3333

; TELEFAX: (212) 840-0712

; TELEEX: 425066 CURTMS

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 980 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal

US-08-220-151-5

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Best Local Similarity 20.7%; Pred. No. 1.3; Mismatches 131; Indels 95; Gaps 18;

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## RESULT 3

US-08-413-118-5

; Sequence 5, Application US/08413118

; Patent No. 5688920

; GENERAL INFORMATION:

; APPLICANT: Paoletti, Enzo

; APPLICANT: Limbach, Keith J.

; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF

; TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR

; NUMBER OF SEQUENCES: 128

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Curtis, Morris &amp; Safford, P.C.

; STREET: 530 Fifth Avenue, 25TH FLOOR

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/413,118

; FILING DATE: 29-MAR-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/220,151

; FILING DATE: 30-MAR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: FROMMER, WILLIAM S.

; REGISTRATION NUMBER: 25,506

; REFERENCE/DOCKET NUMBER: 454310-2670

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 840-3333

; TELEFAX: (212) 840-0712

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 980 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal

US-08-413-118-5

Query Match 4.7%; Score 86.5; DB 1; Length 980;

Best Local Similarity 20.7%; Pred. No. 1.3;

Matches 74; Conservative 58; Mismatches 131; Indels 95; Gaps 18;

QY 43 SSRLLRNHRVQATILQDDDEKVVVEESFKAETSTGTETPLEEPNMSSS-----S 93

Db 232 SSKAEYLDRN--IMHAYHDDDEVELDCRPSLQLRGARAWOTTNDTTSYVGMPWRHY 289

QY 94 TSAFETWIKLQGVNVLFDTS-VIKILDTLYRDRTYARFFVLETIARVPYFA----- 145

Db 290 TSTSVNCIVEEARSVPYDSFALSTGDIVYA---SPFYGLRAAARIHNSYAQERFR 345

QY 146 -----FMSVLHMVETFGWRRADYLVKVFHFAESNEMHLLIM 182

Db 346 QVEGYRPRDLDSKLOAEPPVTKNFTTHPVTVSNWNTEKK--VEACTLTWKKEVDE-LVR 402

QY 183 EELGNSWDFRFLAQHI--ATFYFVMTVFLYILSPRMAYHFSECVESHAYETVDKFLKAS 241

Db 403 DEFEGSY----RTFIRISSTFISNTQFKLESAP-----LTECVSKKEAKAIDSIYKKQ 453

QY 242 GEELKNMPPADIAVKY--TGGDLYLDFEQTSTPTNTRPVLEN-LYDVFVNIRDDAE 298

Db 454 YESTHVFSGD---VEYVLARGGFLIAF-----RPLMSNELARLYLN----- 491



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; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/863.169A
; FILING DATE: 03-APR-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/822.011
; FILING DATE: 19-JAN-1992
; CLASSIFICATION: 530
; APPLICATION NUMBER: US 07/937.893
; FILING DATE: 18-APR-1991
; CLASSIFICATION: 530
; APPLICATION NUMBER: US 615.715
; FILING DATE: 20-NOV-1990
; CLASSIFICATION: 530
; APPLICATION NUMBER: US 510.706
; FILING DATE: 18-APR-1990
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:297/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-863-169A-5

Query Match 4.5%; Score 82.5; DB 1; Length 379;
Best Local Similarity 18.5%; Pred. No. 0.76;
Matches 70; Conservative 67; Mismatches 137; Indels 105; Gaps 17;

QY 2 AAISGSSGTLTISRPLVTLRRSRA-----AVSYSSSHRLLHLLPLSSRRLLLRNHRV 55
Db 46 AVASPMDDGFSVLSDFSVLYRDRAEWADIDVPQDGNPVPVQIIYSK---FRVDYD 102
QY 56 QATILQDDDEKVVVEESFKAETSTGTPELEPNMSSSTSAFETWIK-----LEQGVNV 110
Db 103 FRAVLQDERS---ERAFKL-----TRDAIELNAANYTVWHFRRVLLKSLQKDLHEEMN- 153
QY 111 FLTDSVIKILDTLDRDYARFV-----LETTARVPYFAPMSVLHM-YETFGWNR 160
Db 154 YIT-AIIIEQPKNYQVWHRRVLVLEWRDPSQOELEFIA-----DILNODAKNYHAWQ 204
QY 161 RADYLVKVFHAEASNEMHLL--LIMEELGNSWDFRFLAQHIAATFYFMTVFLYILSPRM 218
Db 205 HRQWVIOEFLKWDNELQYVDQLLKEDVRNNSVWNRQY-----FVISNTT 248
QY 219 AVHFSECVESHAYETDYKFLKASGEELKNMPADIAVKYITGGDLYLDFEFQTSRTPNTR 278
Db 249 GYNDRAVLEREVOYTL-----EMIKLVPHNESAWNLYLKG-----ILQDRGLSKYPNLL 296
QY 279 RPVIE-----NLYDVFVNIRDEAEH-----CKTMRACOTLG----- 310
Db 297 NOLLDLQSHSSPYLIAFLVDIYEDMLNQCNDKEDILNKALELCEITLAKETIRKEYW 356
QY 311 -----SLRSPHSILDDDT 324
Db 357 RYIGRSLOKSHSTENDSPT 375
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RESULT 7
US-08-424-268-8
; Sequence 8, Application US/08424268
; Patent No. 5821118
; GENERAL INFORMATION:
; APPLICANT: Omer, Charles A
; APPLICANT: Diehl, Ronald E
; APPLICANT: Gibbs, Jackson B
; APPLICANT: Kohl, Nancy E
; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Metck & Co., Inc.
; STREET: P.O.Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Power Mac
; OPERATING SYSTEM: System 7.5.3
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,268
; FILING DATE: 4/24/95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 18858PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3903
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; US-08-424-268-8

Query Match 4.5%; Score 82.5; DB 2; Length 379;
Best Local Similarity 18.5%; Pred. No. 0.76;
Matches 70; Conservative 67; Mismatches 137; Indels 105; Gaps 17;

QY 2 AAISGSSGTLTISRPLVTLRRSRA-----AVSYSSSHRLLHLLPLSSRRLLLRNHRV 55
Db 46 AVASPMDDGFSVLSDFSVLYRDRAEWADIDVPQDGNPVPVQIIYSK---FRVDYD 102
QY 56 QATILQDDDEKVVVEESFKAETSTGTPELEPNMSSSTSAFETWIK-----LEQGVNV 110
Db 103 FRAVLQDERS---ERAFKL-----TRDAIELNAANYTVWHFRRVLLKSLQKDLHEEMN- 153
QY 111 FLTDSVIKILDTLDRDYARFV-----LETTARVPYFAPMSVLHM-YETFGWNR 160
Db 154 YIT-AIIIEQPKNYQVWHRRVLVLEWRDPSQOELEFIA-----DILNODAKNYHAWQ 204
QY 161 RADYLVKVFHAEASNEMHLL--LIMEELGNSWDFRFLAQHIAATFYFMTVFLYILSPRM 218
Db 205 HRQWVIOEFLKWDNELQYVDQLLKEDVRNNSVWNRQY-----FVISNTT 248
QY 219 AVHFSECVESHAYETDYKFLKASGEELKNMPADIAVKYITGGDLYLDFEFQTSRTPNTR 278
Db 249 GYNDRAVLEREVOYTL-----EMIKLVPHNESAWNLYLKG-----ILQDRGLSKYPNLL 296
QY 279 RPVIE-----NLYDVFVNIRDEAEH-----CKTMRACOTLG----- 310
Db 297 NOLLDLQSHSSPYLIAFLVDIYEDMLNQCNDKEDILNKALELCEITLAKETIRKEYW 356
QY 311 -----SLRSPHSILDDDT 324
Db 357 RYIGRSLOKSHSTENDSPT 375
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; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/968,782
; FILING DATE: 10/30/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 18858
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3903
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
;
PCT-US93-10442-8

Query Match 4.5%; Score 82.5; DB 5; Length 379;
Best Local Similarity 18.5%; Pred. No. 0.76;
Matches 70; Conservative 67; Mismatches 137; Indels 105; Gaps 17;

QY 2 AAISGSSGTLTISRPLVTLRRSRA-----AVSYSSSHRLLHLLPLSSRRLLRNHRV 55
DB 46 AVASPMDDGFSVLDSPSYLYRDAEWADIDVPONDGPVQIYISDK---FRDVIDY 102
QY 56 QATILQDDEKVVVEFSKAETSTGTEPLEPNMSSSTSAFETWIK-----LEQGVNV 110
DB 103 FRVLQDERS---ERAFKL-----TRDAIELNAANYVWHFRRVLLKSLQKDLHEEN- 153
QY 111 FLTDSVIKILDTLYRDRTYARFV-----LETIARVPYFAFMSVLHM-YETFGWR 160
DB 154 YIT-AITIEOPKQNVQVWHRRVLEWLRDPSQELEFIA-----DILNODAKNYHAWQ 204
QY 161 RADYLKVHFAESNMHHL--LIMEELGNSWDFRFLAQHIATFYFMTVFLYLSPRM 218
DB 205 HRQWVIOEFKLDNELOYVDQLLKEDVRNNSVWQRY-----FVISNTT 248
QY 219 AYHSECVESHAYETYDKFLKASGEELKNMPADIAVKYTTGGDLYLDFEQTSTPNTR 278
DB 249 GYNDRAVLEREVOYTL-----EMIKLVPHNESAWNLYKG---ILQDRGLSKYPNLL 296
QY 279 RPVIE-----NLYDFVFNIRDEAEH-----CKTMRACQTLG----- 310
DB 297 NOLLDLQPSHSPYLIATFLVDIYEDMLENQCDNKEDILNKALELCEILAKEDTIRKEYW 356
QY 311 ----SLRSPHSILDDDDT 324
DB 357 RYIGRSLSQKSHSTENDSPT 375

RESULT 12
US-08-424-268-20
; Sequence 20, Application US/08424268
; Patent No. 5821118
; GENERAL INFORMATION:
; APPLICANT: Omer, Charles A
; APPLICANT: Diehl, Ronald E
; APPLICANT: Gibbs, Jackson B
; APPLICANT: Kohl, Nancy E
; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
; TITLE OF INVENTION: Transferase
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
```

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;
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Power Mac
; OPERATING SYSTEM: System 7.5.3
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,268
; FILING DATE: 4/24/95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 18858PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3903
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
;
US-08-424-268-20

Query Match 4.5%; Score 82.5; DB 2; Length 819;
Best Local Similarity 18.5%; Pred. No. 2.7;
Matches 70; Conservative 67; Mismatches 137; Indels 105; Gaps 17;

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DB 486 AVASPMDDGFSVLDSPSYLYRDAEWADIDVPONDGPVQIYISDK---FRDVIDY 542
QY 56 QATILQDDEKVVVEFSKAETSTGTEPLEPNMSSSTSAFETWIK-----LEQGVNV 110
DB 543 FRVLQDERS---ERAFKL-----TRDAIELNAANYVWHFRRVLLKSLQKDLHEEN- 593
QY 111 FLTDSVIKILDTLYRDRTYARFV-----LETIARVPYFAFMSVLHM-YETFGWR 160
DB 594 YIT-AITIEOPKQNVQVWHRRVLEWLRDPSQELEFIA-----DILNODAKNYHAWQ 644
QY 161 RADYLKVHFAESNMHHL--LIMEELGNSWDFRFLAQHIATFYFMTVFLYLSPRM 218
DB 645 HRQWVIOEFKLDNELOYVDQLLKEDVRNNSVWQRY-----FVISNTT 688
QY 219 AYHSECVESHAYETYDKFLKASGEELKNMPADIAVKYTTGGDLYLDFEQTSTPNTR 278
DB 689 GYNDRAVLEREVOYTL-----EMIKLVPHNESAWNLYKG---ILQDRGLSKYPNLL 736
QY 279 RPVIE-----NLYDFVFNIRDEAEH-----CKTMRACQTLG----- 310
DB 737 NOLLDLQPSHSPYLIATFLVDIYEDMLENQCDNKEDILNKALELCEILAKEDTIRKEYW 796
QY 311 ----SLRSPHSILDDDDT 324
DB 797 RYIGRSLSQKSHSTENDSPT 815

RESULT 13
PCT-US93-10442-20
; Sequence 20, Application PC/TUS9310442
; GENERAL INFORMATION:
; APPLICANT: Omer, Charles A
; APPLICANT: Diehl, Ronald E
; APPLICANT: Gibbs, Jackson B
; APPLICANT: Kohl, Nancy E
; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
; TITLE OF INVENTION: Transferase
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
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Db 79 LLIQNLHRI-----DEEGKKHVALIENLLRRQIGTRSPTEVEICTKPEILFTLMAGYE 132  
Qy 99 TW--IIKLEQGVNVLTDVSIKILDTLYRDTVAREFVLETIARVPVFAFMSVLHMYETF 156  
Db 133 DAHPEIALNSGTML-----RECARV---EALAKI-----MLHSDEFF 166  
Qy 157 GWRRRADYLVHFA-----ESWNEM---HLLIMEELGGSWDFDRFLAQHIATFYFMTV 209  
Db 167 KFRYVEVSTFDIASDAFSTFKELLTRHKLCAEFLDAN---YDKFFSQ----- 212  
Qy 210 FLYILSPRMAYHFSECVEHAYETYDKFLKASGEELKNMPADIAVXYTGGD-LYL--- 265  
Db 213 -----HYQRLNSENHYVTRQSLKLLGELLDRHNTVMTRYISEPENLKLMMN 261  
Qy 266 -----FDEFQTSR---TNTRRPVIE-----NLYDVFNIRDEAE 298  
Db 262 MLKEKSRNIQFEAPHVFKVFNANPKPKPILDLILRNQTKLVDFELTNFHTDRSE 315

Search completed: February 2, 2003, 22:49:18  
Job time : 28 secs



GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: February 2, 2003, 22:46:20 ; Search time 18 Seconds

(without alignments)  
393.482 Million cell updates/sec

Title: US-09-807-867-2

Perfect score: 1845

Sequence: 1 MAALSGISGTLTISRPLVT.....VPEAHCEGIVCLKRSITS 351

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database : Published\_applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
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7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
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13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description         |
|------------|-------|---------------|--------|-------|---------------------|
| 1          | 96    | 5.2           | 917    | 10    | US-09-815-242-5603  |
| 2          | 96    | 5.2           | 920    | 10    | US-09-815-242-12181 |
| 3          | 96    | 5.2           | 920    | 10    | US-09-815-242-12995 |
| 4          | 96    | 5.2           | 920    | 10    | US-09-815-242-13148 |
| 5          | 84.5  | 4.6           | 1881   | 9     | US-09-998-425-3     |
| 6          | 82.5  | 4.5           | 394    | 10    | US-09-925-302-722   |
| 7          | 80.5  | 4.4           | 608    | 9     | US-10-023-437-41    |
| 8          | 80.5  | 4.4           | 2139   | 10    | US-09-727-384-6     |
| 9          | 80    | 4.3           | 599    | 10    | US-09-952-013A-4    |
| 10         | 79.5  | 4.3           | 183    | 10    | US-09-801-574-70    |
| 11         | 78.5  | 4.3           | 1167   | 10    | US-09-815-242-11522 |
| 12         | 78    | 4.2           | 572    | 9     | US-10-025-222A-39   |
| 13         | 78    | 4.2           | 902    | 9     | US-09-922-199A-2    |
| 14         | 77.5  | 4.2           | 377    | 10    | US-09-935-390A-31   |
| 15         | 77    | 4.2           | 458    | 10    | US-09-742-582-11    |
| 16         | 75.5  | 4.1           | 217    | 10    | US-09-841-132-403   |
| 17         | 75.5  | 4.1           | 396    | 10    | US-09-925-297-629   |
| 18         | 75.5  | 4.1           | 876    | 9     | US-09-712-363-243   |
| 19         | 75    | 4.1           | 231    | 9     | US-09-738-626-6594  |

20 75 4.1 328 9 US-10-028-072-34 Sequence 34, Appl  
21 75 4.1 356 9 US-10-120-319-12 Sequence 12, Appl  
22 75 4.1 418 9 US-09-832-659-42 Sequence 42, Appl  
23 75 4.1 450 9 US-09-738-626-3752 Sequence 3752, Ap  
24 74.5 4.0 755 9 US-09-738-626-4773 Sequence 4773, Ap  
25 74.5 4.0 941 9 US-09-992-598-353 Sequence 353, App  
26 74.5 4.0 941 9 US-09-989-293A-353 Sequence 353, App  
27 74.5 4.0 941 9 US-09-989-735-353 Sequence 353, App  
28 74.5 4.0 941 9 US-09-990-444-353 Sequence 353, App  
29 74.5 4.0 941 9 US-09-989-730-353 Sequence 353, App  
30 74.5 4.0 941 9 US-09-990-436-353 Sequence 353, App  
31 74.5 4.0 941 9 US-09-991-181-353 Sequence 353, App  
32 74.5 4.0 941 9 US-09-993-687-353 Sequence 353, App  
33 74.5 4.0 941 9 US-09-989-734-353 Sequence 353, App  
34 74.5 4.0 941 9 US-10-028-072-464 Sequence 464, App  
35 74.5 4.0 941 9 US-09-997-653-353 Sequence 353, App  
36 74.5 4.0 941 10 US-09-989-723-353 Sequence 353, App  
37 74.5 4.0 941 10 US-09-989-723-353 Sequence 353, App  
38 74.5 4.0 941 10 US-09-989-729-353 Sequence 353, App  
39 74.5 4.0 941 10 US-09-989-727-353 Sequence 353, App  
40 74.5 4.0 941 10 US-09-989-731-353 Sequence 353, App  
41 74.5 4.0 941 10 US-09-989-732-353 Sequence 353, App  
42 74.5 4.0 941 10 US-09-991-073-353 Sequence 353, App  
43 74.5 4.0 941 10 US-09-990-442-353 Sequence 353, App  
44 74.5 4.0 941 10 US-09-991-163-353 Sequence 353, App  
45 74.5 4.0 941 10 US-09-993-604-353 Sequence 353, App

## ALIGNMENTS

RESULT 1  
US-09-815-242-5603  
; Sequence 5603, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: PastSeq for Windows Version 4.0  
; SEQ ID NO 5603  
; LENGTH: 917  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
; US-09-815-242-5603

Query Match 5.2%; Score 96; DB 10; Length 917;  
Best Local Similarity 19.8%; Pred. No. 0.28;

Matches 67; Conservative 44; Mismatches 122; Indels 106; Gaps 13;

|    |     |                                                             |     |
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| QY | 71  | ESFKAETSGCTEPLFEPNMSSSTSAFETWITKLGQVNVFLTDSVIKILDTLYRD-RTY  | 129 |
| Db | 592 | EGKMSKSLGNVTPDQVQKQGADIARLVWSSTDYLAEDVRISDEILKQTSQVYKRIKT   | 651 |
| QY | 130 | AREF-----VLET-----IARVPYFAPMSVLHMVETFGWRRRADIYKV            | 167 |
| Db | 652 | LRPMGLNINDFNPDTSIPESELLEVDVRYLLNRLREFT-ASTINNYENF-----DYLNI | 704 |
| QY | 168 | HFAESNEMHULLIME-----ELGNSWNF---DRFLAQHTATYFPYFMVFLYILSPRM   | 218 |
| Db | 705 | -----FOEQVNFINVLSNIFYLDYGDILLYIEQRDSHIRRSQTVLYQLLDMTKLLAPI  | 759 |
| QY | 219 | AYHFSECVESHAYETYDKFLKASGEELKNMPADIAVKYTGCGDLYLDFEFOFTRTPNTR | 278 |
| Db | 760 | LVHTAEVWSHT-----PHVKEESVHLADMPK-----VVEVDQALLDKWRT-----     | 800 |
| QY | 279 | RPVIENLYDVFNIRDEAEHCKTWR-----ACQTLGSLRSPH                   | 316 |
| Db | 801 | -----FNMRLRDVNRPALETARNEKVIGCKSLEAKVTIASNDKFNASEFLTDFDLH    | 850 |
| QY | 317 | SI-----LDDDDTEESGCVVPEAHCEGIVDC                             | 344 |
| Db | 851 | QLFISQVQWPKLDQDQATAYEHGDIIVIEHADGCKERC                      | 899 |

## RESULT 2

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US-09-815-242-12181
: Sequence 12181, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Kari L.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: TITLE OF INVENTION: Prokaryotes
: FILE REFERENCE: ELITRA.OLIA
: CURRENT APPLICATION NUMBER: US/09/815,242
: CURRENT FILING DATE: 2001-03-21
: PRIORITY APPLICATION NUMBER: 60/191,078
: PRIORITY FILING DATE: 2000-03-21
: PRIORITY APPLICATION NUMBER: 60/206,848
: PRIORITY FILING DATE: 2000-05-23
: PRIORITY APPLICATION NUMBER: 60/207,727
: PRIORITY FILING DATE: 2000-05-26
: PRIORITY APPLICATION NUMBER: 60/242,578
: PRIORITY FILING DATE: 2000-10-23
: PRIORITY APPLICATION NUMBER: 60/253,625
: PRIORITY FILING DATE: 2000-11-27
: PRIORITY APPLICATION NUMBER: 60/257,931
: PRIORITY FILING DATE: 2000-12-22
: PRIORITY APPLICATION NUMBER: 60/269,308
: PRIORITY FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 12181
: LENGTH: 920
: TYPE: PRT
: ORGANISM: Staphylococcus aureus
US-09-815-242-12181

```

```

Query Match 5.2%; Score 96; DB 10; Length 920;
Best Local Similarity 19.8%; Pred. No. 0.28;
Matches 67; Conservative 44; Mismatches 122; Indels 1

QY 71 ESFKAETGTGTEPLEERNMSSSTSAFTWIKLEQGVNVLDSVITDLY
 | | | | | | | | | | | | | | | | | | | | | | | |

```

|    |     |                                                           |     |
|----|-----|-----------------------------------------------------------|-----|
| Db | 595 | EGKKMSKSLGNVTPDQVVKQGADIARLWVSSTDLADVRISDEILKOTSDVYRKIRNT | 654 |
| QY | 130 | ARFF-----VLET-----IARVPFAFMSVLHMVYETFGWRRADYLVK           | 167 |
| Db | 655 | LRFMGLNINDPDTSIPSELLEVDVLLNRLREFT--ASTINNVEF-----DYLNI    | 707 |
| QY | 168 | HFAESNEMHHLLIME-----ELGNSWVF---DRFLAQHTATFYFMTVFLYILSPRM  | 218 |
| Db | 708 | -----YOEQVNFINVLSNPLYDYGKILLYI EORDSHIRRSQTVLYQLVDMTKLAPI | 762 |
| QY | 219 | AYHFSECVSHAYETDKFLKASGEELKNPAPDIAKVYTGDIYLFDEFQTSRTPNTR   | 278 |
| Db | 763 | LVHTAEVWSHT-----PHVKESVHLADMPK-----VVEVDQALLDKWRT-----    | 803 |
| QY | 279 | RPVIENLYDFVNIRODEAEHCKTMR-----ACQTLGSLRSPP                | 316 |
| Db | 804 | -----FNMRLDDVNRALRETKVYIGKSLKAEKVTIASNDKFNASEFLTDFDALH    | 853 |
| QY | 317 | ST-----LDDDDTTEESGCVVPEAHCEGIVDC                          | 344 |
| Db | 854 | OLFIVSOVKVVDKLDDOATAYEHGDIVIEHAGEKCERC                    | 892 |

### RESULT 3

```

US-09-815-242-12995
: Sequence 12995, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Karl L.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: TITLE OF INVENTION: Prokaryotes
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: CURRENT FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 12995
: LENGTH: 920
: TYPE: PRT
: ORGANISM: Staphylococcus aureus
US-09-815-242-12995

```

|    |     |                                                              |        |                 |        |                                      |
|----|-----|--------------------------------------------------------------|--------|-----------------|--------|--------------------------------------|
|    |     | Query Match                                                  | 5.2%   | Score 96;       | DB 10; | Length 920;                          |
|    |     | Best Local Similarity                                        | 19.8%; | Pred. No. 0.28; |        |                                      |
|    |     | Matches                                                      | 67;    | Conservative    | 44;    | Mismatches 122; Indels 106; Gaps 13; |
| QY | 71  | ESFKAETSTGTEPLEEENKSSSISAFEWIIKLEGVNVFTDSVIKLDTLYRD-RTY      | 129    |                 |        |                                      |
|    |     | : : : :   : : :   :   :                                      |        |                 |        |                                      |
| Db | 595 | EKGKMSKLGNVIYPDQVKVKOGKADIARLWVSSTDVLADVRISDEILKTQSDVYRKIRNT | 654    |                 |        |                                      |
|    |     | : : : :   : : :   :   :                                      |        |                 |        |                                      |
| QY | 130 | ARFF-----VLET---IARVPYFAFMSVLHWYTFGWRRRADIYLV                | 167    |                 |        |                                      |
|    |     | : : : :   : : :   :   :                                      |        |                 |        |                                      |

Db 655 LRFMLGNINDFNPDTSIPESSELLEVDYRLNRLREFT-ASTINNYENF-----DYLNI 707  
QY 168 HFAESWNEHHLLIME-----ELGGSWWF---DRFLAQHIAFYFYFMTVFLYLSPRM 218  
Db 708 -----YQEVQNFINVLSNFYLDYKGLDLYIEQDRSHIRSMQTVLYQLVDMTKLLAPI 762  
QY 219 AYHFSECVESHAYETYDKFLKASGEELKNMPADIAVKYTYTGGDLYLDFDEFQTSRTPTNTR 278  
Db 763 LVHTAEVWSHT-----PHVKEESVHLADMPK-----VVEVDQALLDKWRT----- 803  
QY 279 RPVIENLYDVFNIRDDAEHCKTMR-----ACQTLGSLRSRPH 316  
Db 804 -----FMNLRDDVNRALETARNEKVIGKSLEAKVTIASNDKFNASEFLTSFDALH 853  
QY 317 SI-----LDDDDTEESGCVVPEEAHCEGIVDC 344  
Db 854 QLFIVSQVKVVDKLDQATAYEHGDIVIEHADGKERC 892

## RESULT 4

US-09-815-242-13148  
; Sequence 13148, Application US/09815242  
; Patent No. US2002061569A1

; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in  
; Prokaryotes

; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13148  
; LENGTH: 920  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-13148

Query Match 5.2%; Score 96; DB 10; Length 920;  
Best Local Similarity 19.8%; Pred. No. 0.28;  
Matches 67; Conservative 44; Mismatches 122; Indels 106; Gaps 13;

QY 71 ESFKAETSTGTEPLEEPNMSSTSAFETWIKLEQGVNVLTDVSVIKILDTLYRD-RTY 129  
Db 595 EGKMSKSLGNVIVDPQVVYKQKADIARLWVSSTDYADVISDEILKQTSDDVYRKINRT 654  
QY 130 ARFF-----VLET-----IARVPYFAFMSVLHMYETFGWRRADYLVK 167  
Db 655 LRFMLGNINDFNPDTSIPESSELLEVDYRLNRLREFT-ASTINNYENF-----DYLNI 707  
QY 168 HFAESWNEHHLLIME-----ELGGSWWF---DRFLAQHIAFYFYFMTVFLYLSPRM 218

Db 708 -----YQEVQNFINVLSNFYLDYKGLDLYIEQDRSHIRSMQTVLYQLVDMTKLLAPI 762  
QY 219 AYHFSECVESHAYETYDKFLKASGEELKNMPADIAVKYTYTGGDLYLDFDEFQTSRTPTNTR 278  
Db 763 LVHTAEVWSHT-----PHVKEESVHLADMPK-----VVEVDQALLDKWRT----- 803  
QY 279 RPVIENLYDVFNIRDDAEHCKTMR-----ACQTLGSLRSRPH 316  
Db 804 -----FMNLRDDVNRALETARNEKVIGKSLEAKVTIASNDKFNASEFLTSFDALH 853  
QY 317 SI-----LDDDDTEESGCVVPEEAHCEGIVDC 344  
Db 854 QLFIVSQVKVVDKLDQATAYEHGDIVIEHADGKERC 892

## RESULT 5

US-09-998-425-3  
; Sequence 3, Application US/09998425  
; Publication No. US20030008346A1

; GENERAL INFORMATION:  
; APPLICANT: Tavtigian, Paul L.  
; APPLICANT: Myriad Genetics, Inc.  
; TITLE OF INVENTION: MMSC1 - An MMAC1 Interacting Protein  
; FILE REFERENCE: MMSC1 Gene  
; CURRENT APPLICATION NUMBER: US/09/998,425  
; CURRENT FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/233,086  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/071,861  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-20  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3

; LENGTH: 1881  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-998-425-3

Query Match 4.6%; Score 84.5; DB 9; Length 1881;  
Best Local Similarity 22.0%; Pred. No. 11;  
Matches 67; Conservative 41; Mismatches 111; Indels 85; Gaps 14;

QY 74 KATSTGTEPLEEPNMSSTSAFETWIKLEQGVNVLTDVSVIK-ILDTLYRD 126  
Db 451 RKTSSSTSPLEPPDRGTVVPELKPALFTGAVETE--TNVDGEDEELKERIDTLKND 508  
QY 127 RTYARFVLETIARVP-----YFAMSVLHMYETFGWRRADYLVKH 168  
Db 509 NIQA---LEKLEKVPDSPENELKSRWENLLGPDYEVWVATLDT-----QIADDAELQ 557  
QY 169 FAESWNEHHLLIMEELGGSWWFDRFLAQHIAFYFYFMTVF-----LYILSPRMAYH 221  
Db 558 KSKLLPIHTLRGLGEV-----DSFDGHH-----YISSIVSGPVDVTLGLLOPE---- 601  
QY 222 FSECVESHAYETYDKFLKASGEELKNMPADIAVKYTYTGGDLYLDFDE---FQTSRTPTNTR 278  
Db 602 -DELLEVNGMLYCKSRREAVSFLKEVPPPTLVCCRR-----LFDDASVDEPRRTETS 655  
QY 279 RPVIENLYDVFNIRDD-----EAEHCKTMRACQTLGSLRSRPHSLDDDDDEES 328  
Db 656 LPETEVDHNDVNTDEDDGELALWSPEVKIVELVKCKGLG-----FSLDYQDPLDPT 710  
QY 329 GCVV 332  
Db 711 RSVI 714

## RESULT 6

US-09-925-302-722  
; Sequence 722, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 722  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-302-722

Query Match 4.5%; Score 82.5; DB 10; Length 394;  
Best Local Similarity 18.5%; Pred. No. 2;  
Matches 70; Conservative 67; Mismatches 137; Indels 105; Gaps 17;

QY 2 AALSGSSGFLTISRPLVTLRSRA-----AVSYSSSHRLLHLLPLSSRRLLRNHRV 55  
Db 61 AVASPMDDGFVLDSPSYLYDRAEWADIDVPQDGNPVVQIYSDK---FRDVYDY 117  
QY 56 QATVLDDDEKVVVEESFKAETSTGTEPLEEPNMSSSTSAFETWLIK-----LEQGVNV 110  
Db 118 FRAVLQORDERS---ERAFKL-----TRDAIELNAANYTWHFRRVLLKSLQKDLHEEMN- 168  
QY 111 FLTDSVIKILDTLDRDTVARFV-----LETIAVPYFAPMSVLHM-YETFGWVR 160  
Db 169 YIT-AIEEPKNQYQVWHRRVLEWLRDPQSELEFIA-----DILNODAKNYHAWQ 219  
QY 161 RADYLVKVFHAESNMHML--LIMEELGNSWNWDFRFLAQHTATFYFMTVFLYILSPRM 218  
Db 220 HRCWVTOEFLKLDNELQYVDQLKEDVRNNSVWQRY-----FVLSWTT 263  
QY 219 AYHFSCEVSHAYETYDKFLKASGEELKNMPADIAVKYITGGDLYLDFEFQTSRTPNTR 278  
Db 264 GYNDRAVLEREQVYTL-----EMIKLVPHNESAWNLYKG---ILQDRGLSKYPNLL 311  
QY 279 RPVIE-----NLVDVFNVRDDEAH-----CKTWRACQTLG----- 310  
Db 312 NQLLDLPQSHSPYLIAFLVDIYEDMLENQCDNKEDILNKALELCEILAKEKDTIRKEYW 371  
QY 311 -----SLRPSHSLDDDDT 324  
Db 372 RYIGRSLSQSKHSTENDSPT 390

RESULT 7  
US-10-023-437-41  
; Sequence 41, Application US/10023437  
; Publication No. US2002018372A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSTON, STEPHEN A.  
; APPLICANT: STEMKE-HALE, KATHERINE  
; APPLICANT: SYKES, KATHRYN F.  
; APPLICANT: KALTENBOECK, BERNHARD  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID  
; FILE REFERENCE: US/023,437  
; CURRENT APPLICATION NUMBER: US/10/023,437  
; CURRENT FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/225,839  
; PRIOR FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 608  
; TYPE: PRT  
; ORGANISM: Chlamydia psittaci  
US-10-023-437-41

Query Match 4.4%; Score 80.5; DB 9; Length 608;  
Best Local Similarity 25.0%; Pred. No. 5.8;  
Matches 44; Conservative 22; Mismatches 77; Indels 33; Gaps 6;  
QY 73 FKAETSTGTEPLEEPNMSSSTSAFETWLIKQGVNVFLTDSVIKILDTLDRDTYAR 131  
Db 425 FLAETASTLNEMLLMSMLKESDSK-----EEKITI-LTRCLDTIFSTLFR----- 469  
QY 132 FVLETTIARVPYFAPMSVLHMYETFGWVRADYLVKVFHAESNMHMLLIMEELGNSW 191  
Db 470 -----QVLFASFEDYDIHAAEHGVPLTEEYLSSTYKLNQNEFYGEIITFDVLSIEW 521  
QY 192 FDRFLAQHTATFYFMTVFLYILSPRMAYHSECV---ESHAYETYDKFLKASGEE 244  
Db 522 -----ARIPHFYFNFYVYATGIIAALCFLEKILNEDNALNLYNLFUKSGSD 571

RESULT 8  
US-09-727-384-6

; Sequence 6, Application US/09727384  
; Patent No. US2002009851A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Heichman, Karen  
; APPLICANT: Cimborra, Daniel M.  
; APPLICANT: Bush, Angie  
; APPLICANT: Mauck, Kimberly  
; APPLICANT: Bartel, Paul L.  
; TITLE OF INVENTION: Protein-Protein Interactions  
; FILE REFERENCE: 2318-271  
; CURRENT APPLICATION NUMBER: US/09/727,384  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 60/168,377  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: US 60/168,379  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: US 60/185,056  
; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 6  
; LENGTH: 2139  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-727-384-6

Query Match 4.4%; Score 80.5; DB 10; Length 2139;  
Best Local Similarity 24.8%; Pred. No. 35;  
Matches 51; Conservative 22; Mismatches 58; Indels 75; Gaps 12;

QY 157 GWWFRADYLVKVFHAESNMHMLLIMEELG---GNSWNWDFRFLAQHTATFYFMTVFLYI 213  
Db 30 GFHKKIOHVK-----NELCHMLSLEEVAPVLOQTLLQNLNIGR--VHFDQKEALILI 80  
QY 214 LSRPMA--YHFSCEVSHAYETYDKFLKASGEELKNMPADIAV---KYITGGDLY--- 264  
Db 81 LSRTLSNEEFQE-----PDCSLEAQPXKVRGKRYGRR 114  
QY 265 LFDEFQTSRTPNTRPVITENLYDVFNVRDDEA-----EHCKTMRA--CQTLGS 311  
Db 115 SLREFQESVEEFPEVTIVIEPL-----DEEARPSHIPAGDCSEHWKTORSEYEAEQ 166  
QY 312 LR--SPHSILDDDDTEESGCVVPEE 335  
Db 167 LRFWNP-----DOLNASQSGSPFPQ 187

RESULT 9  
US-09-952-013A-4  
; Sequence 4, Application US/09952013A  
; Patent No. US2002014680A1  
; GENERAL INFORMATION:

```

; APPLICANT: GRUMMT, Ingrid
; APPLICANT: VINGRON, Martin
; TITLE OF INVENTION: RNA POLYMERASE I TRANSCRIPTION FACTOR TIF-1A
; FILE REFERENCE: 38485-0007
; CURRENT APPLICATION NUMBER: US/09/952.013A
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: PCT/DE00/00767
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: DE 199 11 992.9
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-09-952-013A-4

Query Match 4.3%; Score 80; DB 10; Length 599;
Best Local Similarity 18.9%; Pred. No. 6.4;
Matches 68; Conservative 56; Mismatches 97; Indels 138; Gaps 18;

QY 7 ISSGTLTISRLPLTLRRSRAVSVSSHRLHLPLSSRLLRNHRVQATILQ----- 61
DB 7 :
QY 62 -DDE-----EKVVVEESFKAETSTGTETPELEPNMSSSSTSAFETWIKLEQGVNVF 111
DB 62 :
QY 61 ALDDKAEGNFAGYEDLRQFAKSDTKAPSSLOQLNLSALT-----CNVS 107
DB 61 :
QY 112 LTDS-----VIKILDLY--RD-----RTYARF--FVLETIARVPYFAFMSVLHMYETFG 157
DB 112 :
QY 108 RLDSSNSLVMSVLDVWVSDESFVRCYTRFLGNLSAQSNIPLVMTMLIQHML----- 163
DB 108 :
QY 158 WMRRADYLVKVFHAFESWNEHHLLIMEELGNSWDFRFLAQHIAFFYFMTVFYILSPR 217
DB 158 :
QY 164 --YRPDSLAIHVEHA-----HMALKVYLELV-----PR 189
DB 164 :
QY 218 M-AVHFSECVSHAVETYDKFLKAGSELKNMPADIAVKYTTGGDLYLDFEQTSTRPN 276
DB 218 :
QY 190 AHSLFYSLILEFFYK--DESLLAQMTYISNV-----LSICEY-----VPS 228
DB 190 :
QY 277 TRRPVNIENLYDVFNIRDEAEHCCKTRACOTGLSLRSPHSILDDDDTEESGCVWPEE 335
DB 277 :
QY 229 IKGPNVLAIDKIIQI-DVEIQ-----VEVDDDDDEEDEVVTD 267
DB 229 :

RESULT 10
US-09-801-574-70
; Sequence 70, Application US/09801574
; Patent No. US20020081592A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Peifeng Jeremy
; APPLICANT: Page, David C.
; TITLE OF INVENTION: Reproduction-Specific Genes
; FILE REFERENCE: 0399.2007-002
; CURRENT APPLICATION NUMBER: US/09/801.574
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/187,518
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/261,557
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-574-70

Query Match 4.3%; Score 79.5; DB 10; Length 183;
Best Local Similarity 35.5%; Pred. No. 1.3;
Matches 33; Conservative 9; Mismatches 36; Indels 15; Gaps 6;

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QY 253 IAVKYVTGGDLYLDFEFTSRTPTNRRPVNIENLYDVFNIRDEAEHC-KTRACOTGLS 311
DB 25 :
DB 25 ITLELYT-SYLYLSMAFYFNRRD-----VALENFFRYFLRLSDDKMEHAQKLMR-----LQN 75
QY 312 LRSPHSILDDDDTEE-----ESGCVVPEEA-HCE 339
DB 312 :
DB 76 LRGGHICLHDIRKPECOGWESGLVAMESAFHLE 108
QY 76 :

RESULT 11
US-09-815-242-11522
; Sequence 11522, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815.242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11522
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11522
```

```

Query Match 4.3%; Score 78.5; DB 10; Length 1167;
Best Local Similarity 18.1%; Pred. No. 24;
Matches 59; Conservative 49; Mismatches 111; Indels 107; Gaps 11;

QY 40 LPLSSRRLLRN-NHRVQATILQ-----DE-----EKVVVEESFKAETS 78
DB 40 :
DB 172 LPALRESEIKNLDEAVKNTNFQNIWVKALKRSHDSSLVDDEAFKFKIKFGDDASNP 231
QY 79 TGTPELEPNMSSSSTSAFETWIKLEQGVNVFLTDSVILKIDTLRYDRTYARFFVLETL 138
DB 79 :
DB 232 DDEELQKDKTEQSSNDPKQAQTLFDAILLODLANAVNMPTKLGDRNYWENFAKT- 290
QY 139 ARVPYAFMSVLHMYETFGWRRADYLVKVFHAFESWNEHHLLIMEELGNSWDFRFLA- 197
DB 139 :
DB 291 -----GNIARTLNER-----LKELFGKNPELFDNFLT 318
QY 198 -----OHIAIFYFYFMTVFYILSPRMAHFSECVSHAYETYDKFL 238
DB 198 :
DB 319 LRGNHQSIKEERALDMLISHIIT----KPIFDAIFGDNKFNPKALDKMWLKLSDGL 374
QY 239 KASGEELKNMPADIAVKYTTGGDLYLDFEFTQ-----SRTPNRRPVNIENLYDVFNIR 294
DB 239 :
DB 375 EGKTKDLKN-----LYESVKTEAARAKSKSQOELIKNLNTFFK---- 414
```











T04907  
 hypothetical protein T10114.90 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-Jun-1999  
 C:Accession: T04907  
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.  
 submitted to the Protein Sequence Database, April 1998  
 A:Reference number: Z15389  
 A:Molecule type: DNA  
 A:Residues: 1-335 <BEV>  
 A:Cross-references: EMBL:AL021712  
 A:Experimental source: cultivar Columbia; BAC clone T10114  
 C:Genetics:  
 A:Map position: 4  
 A:Introns: 50/2; 113/3; 145/1; 183/3; 220/1; 243/1; 267/1  
 A:Note: T10114.90

Query Match 94.3%; Score 1739; DB 2; Length 335;  
 Best Local Similarity 95.2%; Pred. No. 1.5e-147;  
 Matches 334; Conservative 1; Mismatches 0; Indels 16; Gaps 1;

QY 1 MAAGISSGTTISRPVTLRRSAAVSYSSSHRLHLLPLSSRRLLRNHRVOATIL 60  
 |||||  
 DB 1 MAAGISSGTTISRPVTLRRSAAVSYSSSHRLHLLPLSSRRLLRNHRVOATIL 60  
 |||||  
 QY 61 QDDEKVVVEESFKATSTGTGTEPLEEPNMSSTSAFETWIKLEQGVNVLTDVSKIL 120  
 |||||  
 DB 61 QDDEKVVVEESFKATSTGTGTEPLEEPNMSSTSAFETWIKLEQGVNVLTDVSKIL 120  
 |||||  
 QY 121 DTLYRDTYARFVLETIARVPYFAPMSVLHMYETFGWWRADYLVKVFHAFSWNEMHLL 180  
 |||||  
 DB 121 DTLYRDTYARFVLETIARVPYFAPMSVLHMYETFGWWRADYLVKVFHAFSWNEMHLL 180  
 |||||  
 QY 181 IMEELGNSWDFRFLAQHIAFYFMTVFLYILSPRAYHFSECVESHAYETVDKFLKA 240  
 |||||  
 DB 181 IMEELGNSWDFRFLAQHIAFYFMTVFLYILSPRAYHFSECVESHAYETVDKFLKA 240  
 |||||  
 QY 241 SGEELKNMPADIAKYTYGGLDYLFDEFQTSRTPTNTRPVNIENLYDVFNIRDEAEHC 300  
 |||||  
 DB 241 SGEELKNMPADIAKYTYGGLDYLFDEFQTSRTPTNTRPVNIENLYDVFNIRDEAEHC 300  
 |||||

RESULT 3  
 AB2068  
 oxidase [imported] - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp.  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
 C:Accession: AB2068  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriquchi  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AB2068  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-230 <KUR>  
 A:Cross-references: GB:BA000019; PIDN:BAB73795.1; PTD:gl7131187; GSPDB:GN00179  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: all2096

Query Match 39.1%; Score 721; DB 2; Length 230;  
 Best Local Similarity 60.0%; Pred. No. 8.4e-57;  
 Matches 132; Conservative 34; Mismatches 44; Indels 10; Gaps 12;

QY 101 IIKLEQGVNVLTDVSKILDTLYRDTYARFVLETIARVPYFAPMSVLHMYETFGWR 160

Db 1 MIRLLVGLVLF-----VINTVYDRPYPRFYVLETVARVPYFSYLSVLHLYETLGMWR 53  
 QY 161 RADYLVKVFHAFSWNEMHLLIMEELGNSWDFRFLAQHIAFYFMTVFLYILSPRAYH 220  
 |||||  
 Db 54 KADWLKVFHAFSWNEMHLLIMEELGNSWDFRFLAQHIAFYFMTVFLYILSPRAYH 113  
 |||||  
 QY 221 HFSECVESHAYETVDKFLKASGEELKNMPADIAKYTYGGLDYLFDEFQTSRTPTNTRRP 280  
 |||||  
 Db 114 NFMEQVEQHAYSSYDKFLTTHEAEKLTQPAPEVAKTYIRGDLVMEDEFQTAHSPSPRRP 173  
 |||||  
 QY 281 VIENLYDVFNIRDEAEHCCTMRACOTLG---SLRSPHS 317  
 |||||  
 Db 174 NIDNLYDVFNIRDEAEHCCTMRACOTLG---SLRSPHS 213  
 |||||

## RESULT 4

T08850  
 alternative respiratory pathway oxidase (EC 1.-.-) Aox2 - soybean  
 C:Species: Glycine max (soybean)  
 C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 12-Nov-1999  
 C:Accession: T08850  
 R:Finnegan, P.M.; Whelan, J.; Millar, A.H.; Zhang, Q.; Smith, M.K.; Wiskich, J.T.; Da  
 Plant Physiol. 118, 675-682, 1998  
 A:Title: Differential expression of the multigene family encoding the soybean mitocho  
 A:Reference number: Z16494  
 A:Accession: T08850  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-333 <FIN>  
 A:Cross-references: EMBL:U07906; NID:g2769671; PID:g1946336  
 C:Genetics:  
 A:Note: Aox2  
 A:Superfamily: alternative oxidase  
 C:Keywords: oxidoreductase

Query Match 11.3%; Score 208; DB 2; Length 333;  
 Best Local Similarity 28.5%; Pred. No. 9.8e-11;  
 Matches 74; Conservative 35; Mismatches 95; Indels 56; Gaps 10;

QY 65 EKVVEESF-----KAETSTGTEPLEEPNMSSTSAFETWIKLEQGVNVLTDVSKIL 113  
 |||||  
 Db 78 EKVVEESYWGISRPKVVRREDGTE-----WPWNCMPW-ESYRSNVSIDLTAKHVP 127  
 |||||  
 QY 114 ----DSV----IKIL----DTLYRDTYARFVLETIARVPYFAPMSVLHMYETFGWR 161  
 |||||  
 Db 128 KNVLKVAVRTVLLRPTDFFKRRYGCRAMLEIVAAPGVGMVGLLHLSLRKFQOS 187  
 |||||  
 QY 162 ADYLVKVFHAFSWNEMHLLIMEELGNSWDFRFLAQHIAFYFMTVFLYILSPRAYH 221  
 |||||  
 Db 188 GWTIKALLEAEAEERHMLMTMVEL-VKPKWYERLLVLAVQGVFFNAFFVLYILSPKVAHR 246  
 |||||  
 QY 222 FSECVESHAYETVDKFLK--ASGEELKNMPADIAKYTYGGLDYLFDEFQTSRTPTNTR 279  
 |||||  
 Db 247 IVGLEEEAHSTYELKDLSEG-AIENVPAPAIADYW-----RL 286  
 |||||  
 QY 280 PVNIENLYDVFNIRDDAEH 299  
 |||||  
 Db 287 PKDARLKDVITVIRADEAH 306  
 |||||

## RESULT 5

S45035  
 alternative respiratory pathway oxidase (EC 1.-.-) AOMI - mango  
 C:Species: Mangifera indica (mango)  
 A:Variety: cv. Manila  
 C>Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 19-May-2000  
 C:Accession: S45035  
 R:Cruz-Hernandez, A.; Gomez-Lim, M.A.  
 submitted to the EMBL Data Library, May 1994  
 A:Description: Molecular cloning and expression studies of the alternative oxidase fr  
 A:Reference number: S45035  
 A:Accession: S45035

A:Molecule type: mRNA  
A:Residues: 1-274 <CRU>  
A:Cross-references: EMBL:X79329; NID:g488825; PIDN:CAA55892.1; PID:g488826  
C:Genetics:  
C:Gene: aomi 1  
C:Superfamily: alternative oxidase  
C:Keywords: membrane protein; mitochondrial inner membrane; mitochondrion; oxidoreductas

Query Match 10.9%; Score 200.5; DB 2; Length 274;  
Best Local Similarity 30.1%; Pred. No. 3.5e-10;  
Matches 58; Conservative 28; Mismatches 72; Indels 35; Gaps 6;

QY 117 IKIL-----DTLYRDYARFFVLETIARVPVFAFMSVLHM-----YETFGWRRADYLKV 167  
Db 80 VKILRVPTDIFQRYGCGRAMMLETVAAPGVGMGLHLKSLRLEQSGGW-----IKA 134  
QY 168 HFAESWNEHHLLIMEELGGNSWDFRLAQHIATFYFMTVFLYILSPRMAYHFSECV 227  
Db 135 LLEAEANERHMLMTWEL-VQPKYERLLVLAVQGVFFNSFFVLVYLSPKLAHRIVGYLE 193  
QY 228 SHAYETYDKFLK-ASGEELKNPAPDIAVKYTTGGDLILDFEFQTSRTPNTRRPVNIENLY 286  
Db 194 EBAIHSYTELKDIDSGAIKNIPAPAIADYW-----RLPKDATLTK 234  
QY 287 DVFNIRDEAEH 299

Db 235 DVITVVRADAEH 247

## RESULT 6

T04094  
A: alternative respiratory pathway oxidase (EC 1.-.-.-) - common tobacco  
C:Species: Nicotiana tabacum (common tobacco)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-May-2000  
C:Accession: T04094  
R:Vanlerberghe, G.C.; McIntosh, L.  
Plant Physiol. 105, 867-874, 1994  
A:Title: Mitochondrial electron transport regulation of nuclear gene expression. Studies  
A:Reference number: 215205; MUID:94336775; PMID:8058837  
A:Accession: T04094  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-353 <VAN>  
A:Cross-references: EMBL:S71335; NID:g558053; PIDN:AAC60576.1; PID:g558054  
A:Experimental source: cultivar Bright Yellow  
C:Genetics:  
A:Gene: Aox1  
C:Superfamily: alternative oxidase  
C:Keywords: membrane protein; mitochondrial inner membrane; mitochondrion; oxidoreductas

Query Match 10.8%; Score 198.5; DB 2; Length 353;  
Best Local Similarity 24.4%; Pred. No. 7.5e-10;  
Matches 83; Conservative 46; Mismatches 120; Indels 91; Gaps 14;

QY 5 SGISSGTLISRPVTLRRSRAVSYSSSHRLLHPLSSRRLLL-----RNN 52  
Db 33 TGVMSCAAVFMHCVGPNPSEKAVIVM-----VRHFPVMSRSMSMALNDQHKKAEN 86  
QY 53 HRVQATILQD--DEEKVV-----VESFKAETSTGT-----PLEEPN 88  
Db 87 GSAATGGGGGDEKSVSWYGVQPS-KVTKEDGTETWKNCFRPWETKADLSIDLTKHH 145  
QY 89 MSSSSTSAFETWIKLEQGVNVLDSVIKILDTLYRDTYARFFVLETIARVPVFAFMS 148  
Db 146 ATFLDKFAYTVTK-----SLRYPTDIFQRYGCGRAMMLETVAAPGVGM 194  
QY 149 VLTH-----MYETFGWRRADYLKVFHFAESWNEHHLLIMEELGGNSWDFDR---FLAQHI 200  
Db 195 LLHCKSLRFEQSGGW-----IKTLLEAENERHMLMTFMEVAKPN-WYERALVFAVGQV 248  
QY 201 ATFYYPWTVFLYILSPRMAYHFSECVESHAYETYDKFLKASGE-ELKNMPADPIAVKYTT 259  
Db 249 FFNAYEFT---VLLSPKLAHRIVGVLEEAIAHSYTEFLKELDKGNTENVPAPAIADY-- 303

QY 260 GGDLYLDFDEFTSRTPTNTRPVTIENLYDVFNIRDEAEH 299  
Db 304 -----CRLPKDSSTLLDVVLVVRADAEH 326

## RESULT 7

S51278  
A: alternative respiratory pathway oxidase (EC 1.-.-.-) - common tobacco  
C:Species: Nicotiana tabacum (common tobacco)  
C:Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 24-Sep-1999  
C:Accession: S51278  
R:Wheeler, J.; Smith, M.K.; Meijer, M.; Yu, J.W.; Badger, M.R.; Price, G.D.; Day, D.A.  
submitted to the EMBL Data Library, June 1994  
A:Description: Cloning of an additional cDNA for the alternative oxidase in tobacco.  
A:Reference number: S51278  
A:Accession: S51278  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-297 <WHE>  
A:Cross-references: EMBL:X79768; NID:g633599; PIDN:CAA56163.1; PID:g633600  
C:Genetics:  
A:Gene: aox  
C:Superfamily: alternative oxidase  
C:Keywords: membrane protein; mitochondrial inner membrane; mitochondrion; oxidoreduc

Query Match 10.7%; Score 197.5; DB 2; Length 297;  
Best Local Similarity 27.2%; Pred. No. 7.3e-10;  
Matches 65; Conservative 39; Mismatches 82; Indels 53; Gaps 10;

QY 71 ESFKAETSTGTEPLEEPNMSSTSAFETWIK-LEQGVNVLDSVIKILDTLYRDTY 129  
Db 75 ETYKADLSI---DLTKHHAPTFLDKFAYTVKALRYPTDIF-----FQRYG 119  
QY 130 ARFVLETIARVPVFAFMSVLH-----MYETFGWRRADYLKVFHFAESWNEHHLLIMEE 184  
Db 120 CRAMMLETVAAPGVGMGLHLCKSLRFRFQSGW-----IKALLEAENERHMLMTFME 174  
QY 185 LGGNSWDFDR---FLAQHIATFYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLKAS 241  
Db 175 VAKPN-WYERALVFAVGQVFINAYFT---VLLSPKLAHRIVGVLEEAIAHSYTEFLKEL 230  
QY 242 GE-ELKNMPADPIAVKYTTGGDLILDFEFQTSRTPNTRRPVTIENLYDVFNIRDEAEH 299  
Db 231 DKGNIVNPAPAIADYW-----RLPKDSSTLLDVVLVVRADAEH 270

## RESULT 8

C86448  
A: hypothetical protein F5D14.11 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001  
C:Accession: C86448  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chen, C.W.; Hughes, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
ansen, N.F.; Chung, B.; Huizlar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: C86448  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-318 <STO>  
A:Cross-references: GB:AE005172; NID:g8920609; PIDN:AAF81331.1; GSPDB:GN00141  
C:Genetics:  
A:Map position: 1  
C:Superfamily: alternative oxidase



|                                                                                           |     |                                                               |     |
|-------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------|-----|
| Db                                                                                        | 2   | MSRGATISRSLLI-----COISPRYFSSAAVRGHEPSLIGTSGGTTTFLHGNPGNGSERT  | 57  |
| Qy                                                                                        | 47  | -----LLLRNNRHVOATILQDDEKVVVEESFKATSTGTGP-----LEEPNMSSS        | 92  |
| Db                                                                                        | 58  | ALTWIKLPMRARSASTVATVDQDKDKRDKNGVADGNGKAVVSYWGVEAPKLTKE        | 117 |
| Qy                                                                                        | 93  | S-----TSAFETW-----IIKLEQGVNVFLTDSV-----IKIL-----DPLYRDRTYAR   | 131 |
| Db                                                                                        | 118 | DCTVNRWTCFRPWEYKPDITDLKKHHVPVTLDDKVAFFTVKALRWPDTDLFFQRRYGC    | 177 |
| Qy                                                                                        | 132 | FVLVETIARVPYFAPMSVLH-----MYTFQWRRADYLVKHFAESWNEMHLLIMEELG     | 186 |
| Db                                                                                        | 178 | AMMLETVAAPGVGVMGMLLHCKSLRRFPHSGGW-----IKALLEEAENRMHLMTFMEV-   | 231 |
| Qy                                                                                        | 187 | GNSMWFRD---FLAQHIATFYFMTVFLYILSPRMAYHFSECVESHAYETVDKFLKASGE   | 243 |
| Db                                                                                        | 232 | SPRWTERALFVAVGVGFNFAYFLT---YLASPKLHAIRIVGYLLEEAHISYSEFLNELDK  | 288 |
| Qy                                                                                        | 244 | -ELKNMPADIAPVAVKYYTGGDLYLDFEFQTSRTPNTRRPVNIENLYDVFNIRDDAEH    | 299 |
| Db                                                                                        | 289 | GNIEVPAPATAIDYW-----QMPDPDSTLRDVMVVRADAEALH                   | 326 |
| RESULT 12                                                                                 |     |                                                               |     |
| A46364                                                                                    |     |                                                               |     |
| alternative respiratory pathway oxidase (EC 1.1.3.-) - Arabidopsis thaliana               |     |                                                               |     |
| C:Species: Arabidopsis thaliana (mouse-ear cross)                                         |     |                                                               |     |
| C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999               |     |                                                               |     |
| C:Accession: A46364                                                                       |     |                                                               |     |
| R:Kumar, A.M.; Soll, D.                                                                   |     |                                                               |     |
| A:Title: Arabidopsis alternative oxidase sustains Escherichia coli respiration.           |     |                                                               |     |
| A:Accession: A46364                                                                       |     |                                                               |     |
| A:Status: preliminary; not compared with conceptual translation                           |     |                                                               |     |
| A:Molecule type: nucleic acid                                                             |     |                                                               |     |
| A:Residues: 1-305 <KUM>                                                                   |     |                                                               |     |
| A:Cross-references: GB:G96417; NID:g166875; PIDN:AAA32870.1; PID:g166876                  |     |                                                               |     |
| C:Note: sequence extracted from NCBI backbone (NCBIP:118704)                              |     |                                                               |     |
| C:Superfamily: alternative oxidase                                                        |     |                                                               |     |
| C:Keywords: membrane protein; mitochondrial inner membrane; mitochondrion; oxidoreductase |     |                                                               |     |
| Query Match 10.1%; Score 185.5; DB 2; Length 305;                                         |     |                                                               |     |
| Best Local Similarity 25.1%; Pred. No. 8.9e-09;                                           |     |                                                               |     |
| Matches 59; Conservative 41; Mismatches 90; Indels 45; Gaps 7;                            |     |                                                               |     |
| Qy                                                                                        | 71  | ESFKAETSTGCTPLEEPNMSSSTSAFETWIKLEQGVNVFLTDSVVIKILDTLYRDRTYA   | 130 |
| Db                                                                                        | 83  | ETYKADI---TIDLKHHVPTTFLDRIAYWTVK-----SLRWPTDLFFQRRYGC         | 128 |
| Qy                                                                                        | 131 | REFVLETIARVPYFAPMSVLH-----MYTFQWRRADYLVKHFAESWNEMHLLIMEEL     | 185 |
| Db                                                                                        | 129 | RAMMLETVAAPGVGVMGMLLHCKSLRRFEQSGW-----IKALLEEAENRMHLMTFMEV    | 183 |
| Qy                                                                                        | 186 | GNSMWFRDRLAQHIATFYFMTVFLYILSPRMAYHFSECVESHAYETVDKFLKASGE-E    | 244 |
| Db                                                                                        | 184 | -AKPKWYERALVITVQGVFNAYFLGLYISPKFAHRMVGYLEEEAHSYTEFLKELDKGN    | 242 |
| Qy                                                                                        | 245 | LKNMPADIAPVAVKYYTGGDLYLDFEFQTSRTPNTRRPVNIENLYDVFNIRDDAEH      | 299 |
| Db                                                                                        | 243 | IENVPAPATAIDYW-----RLPADATLRDVMVVRADAEAH                      | 278 |
| RESULT 13                                                                                 |     |                                                               |     |
| T51615                                                                                    |     |                                                               |     |
| alternative respiratory pathway oxidase (EC 1.1.3.-) [similarity] - Arabidopsis thaliana  |     |                                                               |     |
| C:Species: Arabidopsis thaliana (mouse-ear cross)                                         |     |                                                               |     |
| C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000               |     |                                                               |     |
| C:Accession: T51615                                                                       |     |                                                               |     |
| R:Lacomme, C.J.; Roby, D.                                                                 |     |                                                               |     |
| FEB5 Lett. 459, 149-153, 1999                                                             |     |                                                               |     |
| A:Title: Identification of new early markers of the hypersensitive response in Arabidops  |     |                                                               |     |
| Query Match 9.2%; Score 169.5; DB 2; Length 349;                                          |     |                                                               |     |
| Best Local Similarity 28.1%; Pred. No. 2.9e-07;                                           |     |                                                               |     |
| Matches 52; Conservative 27; Mismatches 75; Indels 31; Gaps 5;                            |     |                                                               |     |
| Qy                                                                                        | 121 | DTLYRDRTYARFFVLETIARVPYFAPMSVLH-----YETFGWRRADYLVKHFAESWNE    | 175 |
| Db                                                                                        | 163 | DIFFQRYACRAMMLETVAAPGVGVMGVLHLKLSLRRFEHSGGWIRA-----LLEEANE    | 217 |
| Qy                                                                                        | 176 | MHLLIMEELGNSWFRDLAQHIATFYFMTVFLYILSPRMAYHFSECVESHAYETD        | 235 |
| Db                                                                                        | 218 | RMHLMTFMEV-AOPRWYERALVAVQGVFNAYFLGLYISPKFAHRVVGYLEEAHSY       | 276 |
| Qy                                                                                        | 236 | KFLK-ASGEELKNMPADIAPVAVKYYTGGDLYLDFEFQTSRTPNTRRPVNIENLYDVFNIR | 294 |
| Db                                                                                        | 277 | EFLKDIDNGAIQDCPAPAIADYW-----RLPQGSTLRDVMVTVVRA                | 317 |
| Qy                                                                                        | 295 | DEAEH 299                                                     |     |
| Db                                                                                        | 318 | DEAHH 322                                                     |     |





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OM protein - protein search, using sw model

Run On: February 2, 2003, 22:07:45 ; Search time 22 Seconds  
(without alignments)  
661.736 Million cell updates/sec

Title: US-09-807-867-2

Perfect score: 1845

Sequence: 1 MAATGSSGTLTISRPLVT.....VPEAHCEGIVDCLKRSITS 351

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID        | Description         |
|------------|-------|-------------|--------|--------------|---------------------|
| 1          | 208   | 11.3        | 333    | 1 AOX2_SOYBN | 041266 glycine max  |
| 2          | 200.5 | 10.9        | 297    | 1 AOX2_TOBAC | Q40578 nicotiana t  |
| 3          | 200.5 | 10.9        | 318    | 1 AOX1_MANIN | Q40294 mangifera i  |
| 4          | 196.5 | 10.8        | 353    | 1 AOX1_TOBAC | Q41224 nicotiana t  |
| 5          | 194.5 | 10.5        | 353    | 1 AOX2_ARATH | Q22049 arabidopsis  |
| 6          | 190.5 | 10.3        | 326    | 1 AOX2_SOYBN | Q03376 glycine max  |
| 7          | 189   | 10.2        | 321    | 1 AOX1_SOYBN | Q07185 glycine max  |
| 8          | 187.5 | 10.2        | 329    | 1 AX1C_ARATH | Q22048 arabidopsis  |
| 9          | 185.5 | 10.1        | 354    | 1 AX1A_ARATH | Q39219 arabidopsis  |
| 10         | 176.5 | 9.6         | 325    | 1 AX1B_ARATH | Q23913 arabidopsis  |
| 11         | 169.5 | 9.2         | 349    | 1 AOX1_SAUGU | P22185 saurumatum   |
| 12         | 163   | 8.8         | 351    | 1 AOX_ASPNG  | Q74180 aspergillus  |
| 13         | 153.5 | 8.3         | 342    | 1 AOX_HANAN  | Q00912 hansenua a   |
| 14         | 141.5 | 7.7         | 362    | 1 AOX_NEUCR  | Q01355 neurospora   |
| 15         | 111.5 | 6.0         | 345    | 1 AOX_TRVBB  | Q26710 trypanosoma  |
| 16         | 103.5 | 5.6         | 1920   | 1 PCNT_MOUSE | P48725 mus musculus |
| 17         | 101.5 | 5.5         | 326    | 1 HEM2_PASMU | P57874 pasteurella  |
| 18         | 96    | 5.2         | 917    | 1 SY1_STAUA  | P41972 staphylococ  |
| 19         | 93.5  | 5.1         | 916    | 1 SCRB_LIMPO | Q25386 limulus pol  |
| 20         | 93    | 5.0         | 1174   | 1 EX5B_BUCAI | P57529 buchnera ap  |
| 21         | 91    | 4.9         | 736    | 1 VP4_ROTFC  | P26193 porcine rot  |
| 22         | 90    | 4.9         | 624    | 1 PSAB_AMPCL | P58383 amphidinium  |
| 23         | 89.5  | 4.9         | 979    | 1 VGLB_HSVEL | P25218 equine herp  |
| 24         | 88.5  | 4.8         | 967    | 1 CAP1_SOYBN | Q02909 glycine max  |
| 25         | 88    | 4.8         | 921    | 1 SY1_BACSU  | Q45477 bacillus su  |
| 26         | 87.5  | 4.7         | 437    | 1 FLHE_TREPA | Q56339 treponema p  |
| 27         | 87.5  | 4.7         | 653    | 1 MTS1_STRSA | P29347 streptococ   |
| 28         | 87.5  | 4.7         | 980    | 1 VGLB_HSVEA | P18551 equine herp  |
| 29         | 87.5  | 4.7         | 980    | 1 VGLB_HSVEB | P28922 equine herp  |
| 30         | 87    | 4.7         | 590    | 1 PEPE_BORBU | O51264 borrelia bu  |
| 31         | 87    | 4.7         | 956    | 1 SY1_AQUAE  | O66651 aquifex aeo  |
| 32         | 86.5  | 4.7         | 980    | 1 VGLB_HSVEL | P18050 equine herp  |
| 33         | 86    | 4.7         | 272    | 1 CAT5_YEAST | P41735 saccharomyc  |

34 85.5 4.6 2131 1 YCF2\_SPIOL P08973 spinacia ol  
35 85 4.6 633 1 NOF1\_DROME P15296 drosophila  
36 85 4.6 960 1 CAP2\_SORBI P29194 sorghum bic  
37 85 4.6 960 1 CAP3\_SORBI P15804 sorghum bic  
38 85 4.6 966 1 CAP1\_MESCR P10490 mesembryant  
39 85 4.6 967 1 CAP2\_MAIZE P51059 zea mays (m  
40 85 4.6 984 1 NOF\_DROME P16320 drosophila  
41 84.5 4.6 1165 1 SYV\_AQUAE O67411 aquifex aeo  
42 84 4.6 323 1 HEMZ\_HAEIN P43868 haemophilus  
43 84 4.6 377 1 APJ\_RAT Q9Jhg3 rattus norv  
44 84 4.6 687 1 YBGO\_YEAST P34225 saccharomyc  
45 83.5 4.5 356 1 YD6B\_SCHPO Q10323 schizosacch

#### ALIGNMENTS

RESULT 1  
AOX2\_SOYBN  
ID AOX2\_SOYBN STANDARD; PRT; 333 AA.  
AC Q41266;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Alternative oxidase 2, mitochondrial precursor (EC 1.-.-.-).  
GN AOX2.  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE-97336308; PubMed-9193084;  
RA Finnegan P.M., Whelan J., Millar A.H., Zhang Q., Smith M.K.,  
RA Wiskich J.T., Day D.A.;  
RT "Differential expression of the multigene family encoding the soybean  
RT mitochondrial alternative oxidase.";  
RL Plant Physiol. 114:455-466(1997).  
RN [2]  
RP SEQUENCE OF 206-245 FROM N.A.  
RX MEDLINE-96165778; PubMed-8580775;  
RA Whelan J., Millar A.H., Day D.A.;  
RT "The alternative oxidase is encoded in a multigene family in  
RT soybean.";  
RL Planta 198:197-201(1996).  
CC -!- FUNCTION: CATALYZES CYANIDE-RESISTANT OXYGEN CONSUMPTION. MAY  
CC INCREASE RESPIRATION WHEN THE CYTOCHROME RESPIRATORY PATHWAY IS  
CC RESTRICTED, OR IN RESPONSE TO LOW TEMPERATURES (BY SIMILARITY).  
CC -!- PATHWAY: Alternative respiratory pathway.  
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).  
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL, POSSIBLY IN THE INNER SURFACE  
CC OF THE INNER MITOCHONDRIAL MEMBRANE.  
CC -!- SIMILARITY: BELONGS TO THE ALTERNATIVE OXIDASE FAMILY.  
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CC  
CC EMBL: U87906; AAB97285.1; -  
CC InterPro: IPR002680; AOX.  
CC Pfam: PF01786; AOX; 1.  
KW Oxidoreductase; Transit peptide; Mitochondrion; Respiratory chain;  
FT Inner membrane; Transmembrane; Multigene family.  
FT TRANSIT 1 ?  
FT CHAIN ? 333  
FT TRANSMEM 158 178  
FT TRANSMEM 220 240  
FT POTENTIAL.



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EMBL: X79329; CAA55892.1; ALT\_INIT.  
InterPro: IPR002680; AOX.  
Pfam: PF01786; AOX; 1.

Oxidoreductase; Transit peptide; Mitochondrion; Respiratory chain;  
Inner membrane; Transmembrane.

TRANSIT 1 ? MITOCHONDRION (POTENTIAL).  
CHAIN 318 ALTERNATIVE OXIDASE.  
TRANSMEM 143 163 POTENTIAL.  
TRANSMEM 205 225 POTENTIAL.  
DISULFID 91 91 INTERCHAIN (POTENTIAL).  
METAL 109 109 POTENTIAL.  
METAL 162 162 POTENTIAL.  
METAL 189 189 POTENTIAL.  
METAL 230 230 POTENTIAL.  
METAL 291 291 POTENTIAL.  
METAL 296 296 POTENTIAL.  
SEQUENCE 318 AA; 36640 MW; BILDADZDD6F03E0 CRC64;

Query Match 10.9%; Score 200.5; DB 1; Length 318;  
Best Local Similarity 30.1%; Pred. No. 1.7e-09;  
Matches 58; Conservative 28; Mismatches 72; Indels 35; Gaps 6;

QY 117 IKIL-----DTLYRDTYARFFVLETIARVPYAFMSVLHM-----YETFGWRRADYLKV 167  
DB 124 VILRPVPTDIFQRYGCGRAMLETVAAPGVGMGLHLKSLRKLQSGW-----IKA 178  
QY 168 HFAEENEMHLLIMEELGGNSWFDRLAQHATFYFYFMTVFLYLSPRMAYHFSECV 227  
DB 179 LLEAEENEMHLMTWVQL-VQPKWTERLLVAVQGVFNSFFVLYLSPKLAHRIVGYLE 237  
QY 228 SHAYETYDKFLK-ASGEELKNMPPADIAVKYTYTGGDLYLDFEFQTSRTPNTRRPVNIENLY 286  
DB 238 EEAHSYTEYLKIDISGAIKNIPAPAIADYW-----RLPKDATLK 278  
QY 287 DVFVNIRDEAEH 299  
DB 279 DVTIVVRADEAHH 291

RESULT 4  
AOX1\_TOBAC  
ID AOX1\_TOBAC STANDARD; PRT; 353 AA.  
AC Q41224;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Alternative oxidase 1, mitochondrial precursor (EC 1.-.-.-).  
GN AOX1.  
OS Eucalyptus tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Bright yellow;  
RX MEDLINE=94336775; PubMed=8058837;  
RA Vanlerberghe G.C., McIntosh L.;  
RT "Mitochondrial electron transport regulation of nuclear gene  
expression. Studies with the alternative oxidase gene of tobacco.";  
RL Plant Physiol. 105:867-874(1994).  
CC -!- FUNCTION: CATALYZES CYANIDE-RESISTANT OXYGEN CONSUMPTION. MAY  
INCREASE RESPIRATION WHEN THE CYTOCHROME RESPIRATORY PATHWAY IS  
RESTRICTED, OR IN RESPONSE TO LOW TEMPERATURES (BY SIMILARITY).  
CC -!- PATHWAY: Alternative respiratory pathway.

CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).  
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL, POSSIBLY IN THE INNER SURFACE  
CC OF THE INNER MITOCHONDRIAL MEMBRANE.  
CC -!- SIMILARITY: BELONGS TO THE ALTERNATIVE OXIDASE FAMILY.

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EMBL: S71335; AAC60576.1;  
InterPro: IPR002680; AOX.  
Pfam: PF01786; AOX; 1.  
KW Oxidoreductase; Transit peptide; Mitochondrion; Respiratory chain;  
KW Inner membrane; Transmembrane; Multigene family.  
FT TRANSIT 1 69 MITOCHONDRION (POTENTIAL).  
FT CHAIN 70 353 ALTERNATIVE OXIDASE 1.  
FT TRANSMEM 178 198 POTENTIAL.  
FT TRANSMEM 240 260 POTENTIAL.  
FT DISULFID 126 126 INTERCHAIN (POTENTIAL).  
FT METAL 144 144 POTENTIAL.  
FT METAL 197 197 POTENTIAL.  
FT METAL 224 224 POTENTIAL.  
FT METAL 265 265 POTENTIAL.  
FT METAL 326 326 POTENTIAL.  
FT METAL 331 331 POTENTIAL.  
SQ SEQUENCE 353 AA; 39767 MW; 040C82AEF35E37F CRC64;

Query Match 10.8%; Score 198.5; DB 1; Length 353;  
Best Local Similarity 24.4%; Pred. No. 2.9e-09;  
Matches 83; Conservative 46; Mismatches 120; Indels 91; Gaps 14;

QY 5 SGSSGTLTISRPLVTLRRSRAAVSYSSSRHLHLPLSSRRLL-----RNN 52  
DB 33 TGVMSGAAVFMHGVPAHPSEKAVVTW-----VRHFPVMSGRSAMSALNDKQDKKAEN 86  
QY 53 HRVQATILQD--DEEKV-----VEESFKATSTGT-----PLEEPN 88  
DB 87 GSAATGGGDDGSEKSVSYVGVQPS--KVTKEDGTWKWNCFRPWETKYADLSIDLTKHH 145  
QY 89 MSSSSTSAFETWIKLEQGVNVELTDSVIKILDTLYRDTYARFFVLETIARVPYAFWS 148  
DB 146 APTFDLKPAYTVK-----SLRYPTDIFQRYGCGRAMLETVAAPGVGM 194  
QY 149 VLH-----MYETFGWRRADYLKVHFAESNMHLLIMEELGGNSWFDRL-----FLAQHI 200  
DB 195 LLHCKSLRRPEQSGW-----IKTLLEDAENERMHLMTEVAKPN-WYERALVFAVQGV 248  
QY 201 ATFYFMTVFLYLSPRMAYHFSECVSHAYETYDKFLKASGE-ELKNMPADIAVKYTYT 259  
DB 249 FFNAYFVT-----YLLSPKLAHRIVGYLEEEAHSYTEFLKELDKGNIENVPAPAIADY-- 303  
QY 260 GGDLYLDFEFQTSRTPNTRRPVNIENLYDVFVNIRDEAEH 299  
DB 304 -----CRLPKDSTLLDVVLRVRADEAHH 326

RESULT 5  
AOX2\_ARATH  
ID AOX2\_ARATH STANDARD; PRT; 353 AA.  
AC Q22049;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Alternative oxidase 2, mitochondrial precursor (EC 1.-.-.-).  
GN AOX2 OR AT5G64210 OR MSJ1.5.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.







Best Local Similarity 25.1%; Pred. No. 3.6e-08;  
Matches 59; Conservative 41; Mismatches 90; Indels 45; Gaps 7;

QY 71 ESFKAETSTGTEPLEPNMSSSTSAFETWIKLEQGVNVFLTDSVVIKILDTLYRDRYA 130  
Db 132 EYTKADI---TIDLKHHVPTFLDRIAYTVTK-----SLRWPTDLFFQRYGC 177  
QY 131 RFVLETIARVPYFAPMSVLH-----MYETFGWRRADYLVKVFHFAESWNEHMLIMEEL 185  
Db 178 RAMMLETVAAPGVGMGLHCKSLRRFEQSGW-----IKALLEAEANERHMLTMEV 232  
QY 186 GNSWFWDFRLAQHIAFYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLK-ASGEE 244  
Db 233 -AKPKWYERALVITVQGVFNAYFLGLYLSIPKFAHRMVGYLEEAEIHSYTEFLKELDKGN 291  
QY 245 LKNMPPADIAVYKTYGDLVLFDEFOTSRTPNTRRPVNIENLYDVFNIRDDAEAH 299  
Db 292 IENVPAPAIADYW-----RLPADATLRDVMVVRADAEAH 327

RESULT 10  
AX1B.ARATH STANDARD; PRT; 325 AA.

AC Q23913;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Alternative oxidase 1b, mitochondrial precursor (EC 1.-.-.-).  
GN AOX1B OR AT3G22360 OR MCB17.10.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia; TISSUE=Leaf, and Stem;  
RX MEDLINE=98009993; PubMed=9349280;  
RA Saisho D., Nambara Y., Kaneko T., Katoh T., Asamizu E., Nakazono M.;  
RT "Characterization of the gene family for alternative oxidase from  
Arabidopsis thaliana."  
RL Plant Mol. Biol. 35:585-596(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=20277480; PubMed=10819329;  
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
features of the regions of 4,504,864 bp covered by sixty P1 and TAC  
clones."  
RL DNA Res. 7:131-135(2000).  
CC -!- FUNCTION: CATALYZES CYANIDE-RESISTANT OXYGEN CONSUMPTION. MAY  
INCREASE RESPIRATION WHEN THE CYTOCHROME RESPIRATORY PATHWAY IS  
RESTRICTED, OR IN RESPONSE TO LOW TEMPERATURES (BY SIMILARITY).  
CC -!- PATHWAY: Alternative respiratory pathway.  
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).  
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL, POSSIBLY IN THE INNER SURFACE  
OF THE INNER MITOCHONDRIAL MEMBRANE.  
CC -!- SIMILARITY: BELONGS TO THE ALTERNATIVE OXIDASE FAMILY.  
CC  
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CC  
CC EMBL; D89875; BAA22624.1; .  
CC DR EMBL; AB022215; BAB01774.1; .  
CC DR InterPro; IPR002680; AOX.  
CC DR Pfam; PF01786; AOX; 1.  
CC Oxidoreductase; Transit peptide; Mitochondrion; Respiratory chain;  
KW

Inner membrane; Transmembrane: Multigene family.  
FT TRANSIT 1 44  
FT CHAIN 45 325  
FT TRANSMEM 150 170  
FT TRANSWEM 212 232  
FT DISULFID 98 98  
FT METAL 116 116  
FT METAL 169 169  
FT METAL 196 196  
FT METAL 237 237  
FT METAL 298 298  
FT METAL 303 303  
SQ SEQUENCE 325 AA; 37432 MW; 05B0826FDFB4A1F2 CRC64;

Query Match 9.6%; Score 176.5; DB 1; Length 325;  
Best Local Similarity 24.3%; Pred. No. 1.8e-07;  
Matches 57; Conservative 42; Mismatches 91; Indels 45; Gaps 7;

QY 71 ESFKAETSTGTEPLEPNMSSSTSAFETWIKLEQGVNVFLTDSVVIKILDTLYRDRYA 130  
Db 103 EYTKSDL--TIDLKHHVPTFLDKLAYTVK-----SLRWPTDLFFQRYGC 148  
QY 131 RFVLETIARVPYFAPMSVLH-----MYETFGWRRADYLVKVFHFAESWNEHMLIMEEL 185  
Db 149 RAMMLETVAAPGVGMGLHCKSLRRFEQSGW-----IKALLEAEANERHMLTMEV 203  
QY 186 GNSWFWDFRLAQHIAFYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLK-ASGEE 244  
Db 204 AKPN-WYERALVIAVQGIFFNAYFLGLYLSIPKFAHRMVGYLEEAEIHSYTEFLKELDKGN 262  
QY 245 LKNMPPADIAVYKTYGDLVLFDEFOTSRTPNTRRPVNIENLYDVFNIRDDAEAH 299  
Db 263 IENVPAPAIADYW-----RLPADATLRDVMVVRADAEAH 298

RESULT 11  
AOX1.SAUGU STANDARD; PRT; 349 AA.

AC P22185;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Alternative oxidase, mitochondrial precursor (EC 1.-.-.-).  
GN AOX1.  
OS Sauromatum guttatum (Voodoo lily).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Sauromatium.  
OX NCBI\_TaxID=4463;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 67-75.  
RX MEDLINE=91172765; PubMed=1706518;  
RA Rhoads D.M., McIntosh L.;  
RT "Isolation and characterization of a cDNA clone encoding an  
alternative oxidase protein of Sauromatum guttatum (Schott).";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:2122-2126(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93192522; PubMed=8448361;  
RA Rhoads D.M., McIntosh L.;  
RT "The salicylic acid-inducible alternative oxidase gene aox1 and genes  
encoding pathogenesis-related proteins share regions of sequence  
similarity in their promoters."  
RL Plant Mol. Biol. 21:615-624(1993).  
CC -!- FUNCTION: CATALYZES CYANIDE-RESISTANT OXYGEN CONSUMPTION. MAY  
INCREASE RESPIRATION WHEN THE CYTOCHROME RESPIRATORY PATHWAY IS  
RESTRICTED, OR IN RESPONSE TO LOW TEMPERATURES. IN S.GUTTATUM THE  
ALTERNATIVE RESPIRATORY PATHWAY IS THERMOGENIC.  
CC -!- PATHWAY: Alternative respiratory pathway.  
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).  
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL, POSSIBLY IN THE INNER SURFACE  
OF THE INNER MITOCHONDRIAL MEMBRANE.  
CC -!- INDUCTION: BY SALICYLIC ACID.  
CC -!- MISCELLANEOUS: THE 3 ALTERNATIVE OXIDASE PROTEINS DETECTED IN

S. GUTTATUM, WITH APPARENT MW OF 35 kDa, 36 kDa AND 37 kDa, MAY BE POSTTRANSLATIONALLY MODIFIED PRODUCTS OF THE SAME AOX1 GENE.

-!- SIMILARITY: BELONGS TO THE ALTERNATIVE OXIDASE FAMILY.

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EMBL; M60330; AAA34048.1; -

DR EMBL; Z15117; CAA78823.1; ALT\_SEQ.

DR PIR; A39158; A39158.

DR InterPro; IPR002680; AOX.

DR Pfam; PF01786; AOX; 1.

KW Oxidoreductase; Transmembrane; Mitochondrion; Respiratory chain;

KW Inner membrane; Transmembrane.

FT TRANSIT 1 63 MITOCHONDRION (POTENTIAL).

FT CHAIN 64 349 ALTERNATIVE OXIDASE.

FT TRANSMEM 174 194 POTENTIAL.

FT TRANSMEM 236 256 POTENTIAL.

FT DISULFID 122 122 INTERCHAIN (POTENTIAL).

FT METAL 140 140 POTENTIAL.

FT METAL 193 193 POTENTIAL.

FT METAL 220 220 POTENTIAL.

FT METAL 261 261 POTENTIAL.

FT METAL 322 322 POTENTIAL.

FT METAL 327 327 POTENTIAL.

FT SEQUENCE 349 AA; 38931 MW; 6E70B2B7A858B273 CRC64;

Query Match 9.2%; Score 169.5; DB 1; Length 349;

Best Local Similarity 28.1%; Pred. No. 7.6e-07;

Matches 52; Conservative 27; Mismatches 75; Indels 31; Gaps 5;

QY 121 DTLYDRRTYARFVLETIARVYFAPMSVLHM-----YETFGWRRADYLKVHFAESWNE 175

DB 163 DIFFQRRYACRAMMLETVAAPGVGVVLLHLKSLRFEHSGGWIRA-----LLEAEENE 217

QY 176 MHLIMEELGNSWMDRFLAQHIATFYFTVFLYILSPRMAYHFSECVESHAYETVD 235

DB 218 RHLMTFMEV-AQPRWYERALVAVOGVFNAYFLGYLLSPKFAHVVGYLEEEAIHSIT 276

QY 236 KFLK-ASGEELKNMPPADIAVKYITGGDLYLFDEFQTSRTPTRPVNIENLYDVFVNIRD 294

DB 277 EPLKIDISGAIQDCPAPAIALDYW-----RLPQGSTLRDVTVVVRA 317

QY 295 DEAEH 299

DB 318 DEAHH 322

RESULT 12

AOX\_ASPNG STANDARD; PRT; 351 AA.

AC 074180;

DT 15-JUL-1999 (Rel. 38, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Alternative oxidase, mitochondrial precursor (EC 1.-.-.-).

GN AOX1.

OS Aspergillus niger.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eukotiales; Trichosporaceae; mitosporic Trichosporaceae; Aspergillus.

OX NCBI\_TaxID=5061;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=WU-2223L;

RX MEDLINE=99132188; PubMed=9933359;

RA Kirmura K., Yoda M., Usami S.;

RT "Cloning and expression of the cDNA encoding an alternative oxidase from Aspergillus niger WU-2223L."

RL Curr. Genet. 34:472-477(1999).

CC -!- FUNCTION: CATALYZES CYANIDE-RESISTANT OXYGEN CONSUMPTION. MAY INCREASE RESPIRATION WHEN THE CYTOCHROME RESPIRATORY PATHWAY IS RESTRICTED, OR IN RESPONSE TO LOW TEMPERATURES (BY SIMILARITY).

CC -!- PATHWAY: Alternative respiratory pathway.

CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL, POSSIBLY IN THE INNER SURFACE OF THE INNER MITOCHONDRIAL MEMBRANE (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE ALTERNATIVE OXIDASE FAMILY.

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EMBL; AB016540; BAA32033.2; -

DR InterPro; IPR002680; AOX.

DR Pfam; PF01786; AOX; 1.

KW Oxidoreductase; Transmembrane; Mitochondrion; Respiratory chain;

KW Inner membrane; Transmembrane.

FT TRANSIT 1 351 ALTERNATIVE OXIDASE.

FT CHAIN 146 166 POTENTIAL.

FT TRANSMEM 212 232 POTENTIAL.

FT METAL 98 98 POTENTIAL.

FT METAL 169 169 POTENTIAL.

FT METAL 196 196 POTENTIAL.

FT METAL 237 237 POTENTIAL.

FT METAL 302 302 POTENTIAL.

FT METAL 307 307 POTENTIAL.

FT SEQUENCE 351 AA; 40189 MW; 6307953DF833FD24 CRC64;

Query Match 8.8%; Score 163; DB 1; Length 351;

Best Local Similarity 22.3%; Pred. No. 2.7e-06;

Matches 87; Conservative 61; Mismatches 131; Indels 112; Gaps 19;

QY 11 TLTISRLVTLRRSRAAVSYSSSHRLHH-----LPLSSRRL--LLRNHRVQATILQDD 63

DB 3 SLTATAPI-----RAALPKSYMHIATRNYSGLVIANSGSLVANRHOAGKRFIST 56

QY 64 EEKVVVEESKAEETSTGT-----PLEEPNMSSSTSAFETWII-----KL 104

DB 57 TPKSQIKKEFPPTAPHVKEVETAWHPVYTEQMKGVAIAHRDAKNWADWALGTVMRL 116

QY 105 EOGVNVFLTDSVIKLDLTVR-----DRTYARFVLETIARVYFAPMS 148

DB 117 RWGMD-----LVTGYRHPPGREHARFKMTQKWLTRIFLESVAGVPGWVGGM 166

QY 149 VLMHYETFGWRRADYLKVHFAESWNEHMLIMEELGNSWMDRFL--AQHIATFY 205

DB 167 LRHLRLRRMKRNGWIETLLEAYNERMHLTLFLKL-AEPGWFMRLMVLGAQGV--F 221

QY 206 FMVTVFL-YILSPRMAYHFSECVESHAYETVDKFLKASGEELKNMP-----APDIKVKY 258

DB 222 FNGFFLSYLSMPRICHFRVGYLEEEAVITYTRAIKET--EAGSLPAWEKTEAPEIAVQYW 279

QY 259 TGGDLYLFDEFQTSRTPTRPVNIENLYDVFVNIRDDEAEHCKTMRACOTLGSILR----- 313

DB 280 -----KMPEGOR-----SMKDLLLYVRADEAKH--REVNTLGNLQNAIDP 318

QY 314 SPHSIDDDDEESGCVVPPEAH-CEGIVD 343

DB 319 NPYAAKYKD-----PTKAHPNKGIA 339

RESULT 13

AOX\_HANAN STANDARD; PRT; 342 AA.

ID AOX\_HANAN

AC Q00912;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)









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Db 121 DTLVDRRTYARFVLEETIARVYFAFMSVLMHYETFGWRRADYLKVFHAESENEMHLL 180
QY 181 IMEELGNSWMDRFLAQAHIATFYEMTVFLYLLSPMAVHSECVSHAETTYDKFLKA 240
Db 181 IMEELGNSWMDRFLAQAHIATFYEMTVFLYLLSPMAVHSECVSHAETTYDKFLKA 240
QY 241 SGEELKNMPPADIAVKYTGDLFLDFEPTSTPTNRRPVLENLVDVFNIRDDAEHC 300
Db 241 SGEELKNMPPADIAVKYTGDLFLDFEPTSTPTNRRPVLENLVDVFNIRDDAEHC 300
QY 301 KTRACQTLGSLRSPHSITLDDDDTEESGCVPEEAHCCEIVDCLKKSTIS 351
Db 301 KTRACQTLGSLRSPHSITLDDDDTEESGCVPEEAHCCEIVDCLKKSTIS 351

RESULT 2
Q9ZSQ3 PRELIMINARY; PRT; 351 AA.
AC Q9ZSQ3;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE IMUTANS (Hypothetical 40.6 kDa protein) (T10114.90)
DE (AT4G22260/T10114.90).
GN IM.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Wu D., Wright D.A., Weizel C., Voytas D.F., Rodermel S.R.;
RT "The IMUTANS variegation locus of Arabidopsis defines a mitochondrial
RT alternative oxidase homologue that functions during early chloroplast
RT biogenesis."
RT Plant Cell 0:0-0(1999).
RN (2)
RP SEQUENCE FROM N.A.
RA Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Chung M.K.,
RA Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene T10114.90/AT4G22260 (GI:7269072).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RA Shin P., Brooks S., Chao Q., Chen H., Kim C., Ecker J.;
RT "Full length cDNA sequences of Arabidopsis thaliana.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN (4)
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shim P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene T10114.90/AT4G22260 (GI:7269072).";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN (5)
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
EMBL, AF098072; AAD03599.1; -.

DR EMBL: AF326898; AAC41480.1; -.
DR EMBL: AF324663; AAC40014.1; -.
DR EMBL: AF39717; AAK00399.1; -.
DR EMBL: AY045699; AAK74057.1; -.
DR InterPro: IPR002680; AOX.
DR Pfam: PF01786; AOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 351 AA; 40574 MW; DBA38C9A4EC0EF69 CRC64;

Query Match 99.8%; Score 1841; DB 10; Length 351;
Best Local Similarity 99.7%; Pred. No. 2,2e-163;
Matches 350; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAISGISGTLTISRPLVTLRRSRAVSYSSRRLLHLPLSSRRLLRNHRVQATIL 60
Db 1 MAISGISGTLTISRPLVTLRRSRAVSYSSRRLLHLPLSSRRLLRNHRVQATIL 60
QY 61 ODDEKVVVEESFKAETSTGEPLLEPMMSSSTSAFEWTIKLEGVNFIIDSVIKIL 120
Db 61 ODDEKVVVEESFKAETSTGEPLLEPMMSSSTSAFEWTIKLEGVNFIIDSVIKIL 120
QY 121 DTLVDRRTYARFVLEETIARVYFAFMSVLMHYETFGWRRADYLKVFHAESENEMHLL 180
Db 121 DTLVDRRTYARFVLEETIARVYFAFMSVLMHYETFGWRRADYLKVFHAESENEMHLL 180
QY 181 IMEELGNSWMDRFLAQAHIATFYEMTVFLYLLSPMAVHSECVSHAETTYDKFLKA 240
Db 181 IMEELGNSWMDRFLAQAHIATFYEMTVFLYLLSPMAVHSECVSHAETTYDKFLKA 240
QY 241 SGEELKNMPPADIAVKYTGDLFLDFEPTSTPTNRRPVLENLVDVFNIRDDAEHC 300
Db 241 SGEELKNMPPADIAVKYTGDLFLDFEPTSTPTNRRPVLENLVDVFNIRDDAEHC 300
QY 301 KTRACQTLGSLRSPHSITLDDDDTEESGCVPEEAHCCEIVDCLKKSTIS 351
Db 301 KTRACQTLGSLRSPHSITLDDDDTEESGCVPEEAHCCEIVDCLKKSTIS 351

RESULT 3
Q96631 PRELIMINARY; PRT; 335 AA.
AC Q96631;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE Hypothetical 38.7 kDa protein.
DE T10114.90 OR AT4G22260.
GN T10114.90 OR AT4G22260.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN (1)
RP SEQUENCE FROM N.A.
RA Bevan M., Murphy G., Drost L., Hall C., Hudson S., Ridley P.,
RA Bancroft I., Mewes H.W., Mayer K., Schellner C.;
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL021712; CAB16776.1; -.
DR EMBL: AL161557; CAB79181.1; -.
DR InterPro: IPR002680; AOX.
DR Pfam: PF01786; AOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 335 AA; 38674 MW; 3EE8063B73656B07 CRC64;

Query Match 94.3%; Score 1739; DB 10; Length 335;
Best Local Similarity 95.2%; Pred. No. 6.8e-154;
Matches 334; Conservative 1; Mismatches 0; Indels 16; Gaps 1;

QY 1 MAISGISGTLTISRPLVTLRRSRAVSYSSRRLLHLPLSSRRLLRNHRVQATIL 60

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Db 1 MAALISGSSGLTISRPLVLTLSRAAAYSSSSRHLLHLLPLSSRRLLRNHRVQA1IL 60
Oy 61 OODEKVVVEESFAETSTGTEPLEEPNMSSSTSAFETWIKLEOGNVNLTSTSVKIL 120
Db 61 OODEKVVVEESFAETSTGTEPLEEPNMSSSTSAFETWIKLEOGNVNLTSTSVKIL 120
Oy 121 DTLVDRTRAFEFVLETTARVPYFAFMSVLMHMETFGMWRADYLLKVFASNMEMHLL 180
Db 121 DTLVDRTRAFEFVLETTARVPYFAFMSVLMHMETFGMWRADYLLKVFASNMEMHLL 180
Oy 181 IMEELGNSMWFDRFLAQHIAFTFYFMTVLYILSPRAYHFSECVESHAYETDKELKA 240
Db 181 IMEELGNSMWFDRFLAQHIAFTFYFMTVLYILSPRAYHFSECVESHAYETDKELKA 240
Oy 241 SGEELKNMPADIAVKYTGGLYLFDEFQTSRTNPRPVLENLYDFVNIIRDEAEHC 300
Db 241 SGEELKNMPADIAVKYTGGLYLFDEFQTSRTNPRPVLENLYDFVNIIRDEAEHC 300
Oy 301 KTRACQTLGSLRSPHSLDDDTTEESGCVVPEAHCEGIVDCLKSITS 351
Db 285 KTRACQTLGSLRSPHSLDDDTTEESGCVVPEAHCEGIVDCLKSITS 335

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## RESULT 4

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OyFECC9 PRELIMINARY: PRT: 366 AA.
ID 09FECC9: 09FECC9:
AC 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Plastid quinol oxidase (Plastid terminal oxidase).
GN PROX.
OS Lycopersicon esculentum (tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. VENT CHERRY; TISSUE=LEAF;
RA Bae H., Behringer F., Wetzel C., Rodermel S.;
RT "IMMUTANS and GHOST are plastid quinol oxidases: evidence for a new
RT structural model of the mitochondrial alternative oxidase."
RL submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ATISA CRAIG; AND CV. RUTGER;
RX MEDLINE=20398337; PubMed=10938359;
RA Jose E.M., Simkin A.J., Gaffe J., Laboure A.M., Kuntz M., Carol P.;
RT "A Plastid Terminal Oxidase Associated with Carotenoid Desaturation
RT during Chromoplast Differentiation."
RL Plant Physiol. 123:1427-1436(2000).
DR EMBL: AF302932; AAC18450.1; -
DR EMBL: AF177979; AAG02286.1; -
DR EMBL: AF177980; AAG02287.1; -
DR EMBL: AF302931; AAC18449.1; -
DR InterPro: IPR002680; AOX.
DR Pfam: PF01786; AOX. 1.
SQ SEQUENCE 366 AA: 41977 MM; 38C8D5141CCCA8FA CRC64;

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Query Match 66.7%; Score 1231; DB 10; Length 366;  
 Best Local Similarity 66.3%; Pred. No. 1.9e-106;  
 Matches 242; Conservative 40; Mismatches 57; Indels 26; Gaps 7;

```

Oy 3 ATGSSGSLTISRPLVLT---RSRAVSYSSSHRLHLHLLPL-----SSRLLLRNHR 54
Db 4 S1SASFGTSVSSYSCFRASFEKSSVLCNSQNPFRNSVPIRKSIDGASRCSSVSKSCR 63
Oy 55 VQATLQODEKVVVEESFAETSTGTEPLEEPNMSSSTSAFETWIKLEO 106
Db 64 VQATLQODEKVVVEESFAETSTGTEPLEEPNMSSSTSAFETWIKLEO 117

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Oy 107 GNVNLTDSVYKILDTLYDRDYAFEFVLETTARVPYFAFMSVLMHMETFGMWRADYLLK 166
Db 118 SNVILLTDSVYKILDTLYDRDYAFEFVLETTARVPYFAFMSVLMHMETFGMWRADYLLK 177
Oy 167 VHFASNMENHLLIMEELGNSMWFDRFLAQHIAFTFYFMTVLYILSPRAYHFSECV 226
Db 178 VHFASNMENHLLIMEELGNSMWFDRFLAQHIAFTFYFMTVLYILSPRAYHFSECV 237
Oy 227 ESHAYETDKELKASGEELKNMPADIAVKYTGGLYLFDEFQTSRTNPRPVLENLY 286
Db 238 ESHAYETDKELKASGEELKNMPADIAVKYTGGLYLFDEFQTSRTNPRPVLENLY 297
Oy 287 DVEFNIIRDEAEHCCKTMRACQTLGSLRSPHSLDD-DTEESGCVVPEAHCEGIVDCL 345
Db 298 DVEFNIIRDEAEHCCKTMRACQTLGSLRSPHSLDD-DTEESGCVVPEAHCEGIVDCL 354
Oy 346 KKSIT 350
Db 355 KKSIT 359

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## RESULT 5

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ID 09FZ04 PRELIMINARY: PRT: 357 AA.
AC 09FZ04:
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Plastid terminal oxidase.
GN PROX.
OS Capsicum annuum (bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. YOLO WONDER;
RX MEDLINE=20398337; PubMed=10938359;
RA Jose E.M., Simkin A.J., Gaffe J., Laboure A.M., Kuntz M., Carol P.;
RT "A Plastid Terminal Oxidase Associated with Carotenoid Desaturation
RT during Chromoplast Differentiation."
RL Plant Physiol. 123:1427-1436(2000).
DR EMBL: AF177981; AAG02288.1; -
DR InterPro: IPR002680; AOX.
DR Pfam: PF01786; AOX. 1.
SQ SEQUENCE 357 AA: 41010 MM; 9047B0201A0CTD94 CRC64;

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Query Match 64.6%; Score 1191.5; DB 10; Length 357;  
 Best Local Similarity 69.2%; Pred. No. 9.1e-103;  
 Matches 227; Conservative 38; Mismatches 42; Indels 21; Gaps 5;

```

Oy 29 SYSSSHRLHLLPLSSRRLLRNHRVQA1ILDTLDRDYAFEFVLETTARVPYFAFMSVLMH 81
Db 36 SLRNSHR-----TFQPSLSRKSRRVATLLKENEDEVVERSFAPKSPGNVGGNGNG 88
Oy 82 EPLEEPNMSSSTSAFETWIKLEOGNVNLTSTSVKILDTLDRDYAFEFVLETTARVPYFA 141
Db 89 EPPD-----NSSMNGLEKWKVYIKLEOGNVNLTSTSVKILDTLDRDYAFEFVLETTARVPYFA 143
Oy 142 PYFAFMSVLMHMETFGMWRADYLLKVFASNMENHLLIMEELGNSMWFDRFLAQHIA 201
Db 144 PYFAFMSVLMHMETFGMWRADYLLKVFASNMENHLLIMEELGNSMWFDRFLAQHIA 203
Oy 202 TFYFMTVLYILSPRAYHFSECVESHAYETDKELKASGEELKNMPADIAVKYTGGLY 261
Db 204 VFYFMTVLYILSPRAYHFSECVESHAYETDKELKASGEELKNMPADIAVKYTGGLY 263
Oy 262 DLYLDEFQTSRTNPRPVLENLYDFVNIIRDEAEHCCKTMRACQTLGSLRSPHSLDD 321
Db 264 DLYLDEFQTSRTNPRPVLENLYDFVNIIRDEAEHCCKTMRACQTLGSLRSPHSLDD 322
Oy 322 DTEESGCVVPEAHCEGIVDCLKSI 349

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QY 281 VIENLVDFVNIIRDEAEHCKTMRACOTLG---SLRSPHS 317  
 Db 174 NIDNLYDFVAIRDEDEMEHVKTMVACQOTNAKXSLKSPHN 213

## RESULT 9

Q8S308

PRELIMINARY; PRT; 471 AA.

AC 08S308;  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Quinol-to-oxygen oxidoreductase.  
 OS Chlamydomonas reinhardtii.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Chlamydomonadaceae; Chlamydomonas.  
 OX NCBI\_TaxID=3055;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chen H.-C., Melis A.;  
 RT "A putative chloroplast quinol-to-oxygen oxidoreductase in  
 Chlamydomonas reinhardtii."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF494290; AAM12876.1; -;  
 SQ SEQUENCE 471 AA; 53907 MW; B5754A101D6F0AC8 CRC64;

Query Match 33.6%; Score 619.5; DB 10; Length 471;  
 Best Local Similarity 41.8%; Pred. No. 3,1e-49;  
 Matches 138; Conservative 50; Mismatches 95; Indels 47; Gaps 10;

QY 24 SRAVYSSSHRLHLHPLSRRLRLNNHRQATILDDDEKVVVESEFKAETSTGTE- 82  
 Db 160 SRAA--YVSGQALSDIDAVDRAL-----EAAQVLEPLRPRAVTLDGVTROSESSKLT 210  
 QY 83 -----PLEERNMS-----SSTSAFER-WIKLEQGVNFLTDSVITLD 121  
 Db 211 INNCAEIRSKLQKLELNSKAMMDREHAREQSGRGVETPWLK-----GYVL--SLCLLD 263  
 QY 122 TLYDRYTAFFVETLTAARVPEFAFMSVILHMYETFGWMRR-ADYLVKHFESNMENHLL 180  
 Db 264 FLYERKPLQRFWELETYARMPFYSITSLHLYESLGWMRRACAEIKTHFAFENNELHLL 323  
 QY 181 IMEELGNSMWFDFLQOHATTFYFMTVLYLISPRMAVHSECVSHAYETDKFLKA 240  
 Db 324 IMESIGDQLWFDFAQAHAIILYIILGLYVSPRLAYNFSLLIEYHAVDYGEFWDA 383  
 QY 241 SGEELKNMPADIAVKYTTGDLILPDEPQTSR-TPVTRRVINLYDVFNINDDAEH 299  
 Db 384 NEELKSLPLPLVAAYVYRSODLYMFDSFQTSQMPNRRPSCKTLVDVFNICDDMEH 443  
 QY 300 CKTMACOTLGLSRSPHILDDDDTEESG 329  
 Db 444 VKTKMACO-----DEVOSDITTRREDG 466

RESULT 10  
 Q94G89  
 ID 094G89 PRELIMINARY; PRT; 158 AA.

AC 094G89;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Oxidase (Fragment).  
 GN IM.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Gong J., Chen S.;

RT "Genomic DNA for IM gene from rice."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF241239; AAK70807.1; -;  
 DR InterPro: IPR002680; AOX.  
 DR Pfam: PF01786; AOX; 1.  
 FT NON-TER  
 SQ SEQUENCE 158 AA; 18597 MW; A0D690C05095FA24 CRC64;

Query Match 31.6%; Score 583.5; DB 10; Length 158;  
 Best Local Similarity 68.6%; Pred. No. 1,6e-46;  
 Matches 109; Conservative 21; Mismatches 26; Indels 3; Gaps 2;

QY 193 DRFLAQHIAFTFYFMTVLYLISPRMAVHSECVSHAYETDKFLKASGEELKNMPAD 252  
 Db 1 DRFLARFAAFYFMTVAMVSPRMAVHSECVSHAYETDKFLKHEDELKTKLPAPE 60  
 QY 253 IAVKYYTGDDLYLDFDEFQTSRTPNTRRVINLYDVFNIRDEAEHCKTMRACOTLGL 312  
 Db 61 AALNLYLNEDLYLDFDEFQTSRTPNTRRVINLYDVFNIRDEAEHCKTMRACOTHGL 120  
 QY 313 RSPHSILDDDDTEESGCVPEERAHCEGIVDCIKSITS 351  
 Db 121 RSPHSIMOKCLEDTFE--CVIPED-DCEGIVDCVKSIVS 156

## RESULT 11

Q93X12

PRELIMINARY; PRT; 329 AA.

AC 093X12;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Putative alternative oxidase.  
 GN AOX.  
 OS Vigna unguiculata (Cowpea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae; Vigna.  
 OX NCBI\_TaxID=3917;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. EPACE-1; TISSUE=LEAF;  
 RA Costa J.H., Hasenitz-Saunders M.P., Jolivet Y., Fernandes de Melo D.,  
 RA Pham-Thi A.T., Silva Lima M., Dizengremel P.;  
 RT "Identification and sequencing of two cDNA clones encoding Vigna  
 unguiculata alternative oxidase."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ319899; CAC42836.1; -;  
 DR InterPro: IPR002680; AOX.  
 DR Pfam: PF01786; AOX; 1.  
 SQ SEQUENCE 329 AA; 37650 MW; FFD6F2694FFA9ED7 CRC64;

Query Match 11.2%; Score 207.5; DB 10; Length 329;  
 Best Local Similarity 27.7%; Pred. No. 5,3e-11;  
 Matches 75; Conservative 44; Mismatches 101; Indels 51; Gaps 11;

QY 54 RVQATILDDDEKVV-----VVEESF-----KAETSTGTE-----PLE--EPNMSSSS 93  
 Db 58 QAFAKLPKKEKKEAFAEKSVYESSYWGISRPRIMRBDGTEWNCNMPETVHNSNLSIDL 117  
 QY 94 TSAF--ETWIIKLEGVNVFLDSVYIKLIDTLRYDRTY-ARPPVETARVYFAPMSYL 150  
 Db 118 TKHHVPKNPLDKV----AVRTVKLRIFPTDLFFQRRYCCRAMMETVAAYVGMGMML 172  
 QY 151 HMYETFGWMRRADLYLVKVFHVAESVNEHNLHIMEELGNSMWFDRFLAQHIAFTFYFMTV 210  
 Db 173 HLNSLRKFQDSGGMWIKALIMEAEANERMHMLMTYEL-VKRWTERLLVIAVQGVFNAPFV 231  
 QY 211 LYLISPRMAVHSECVSHAYETDKFLK--ASGEELKNMPADIAVKYTTGDDLYLDFDE 268  
 Db 232 LYTLSPKVAHRIYGYDEELAHSYETDKLDESG-AIENVPAALAIQW----- 280  
 QY 269 FQTSRTPNTRRVINLYDVFNIRDEAEH 299

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Db 281 -----RLEPKDAKLDVTTVTRADEAH 302

RESULT 12
082807 PRELIMINARY; PRT; 332 AA.
AC 082807;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Alternative oxidase.
GN AOX1A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriobacteriota; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NTPRONBARE; TISSUE=CALLUS;
RA MEDLINE=98086211; PubMed=9426242;
RA Ito Y., Saito D., Nakazono M., Tsutsumi N., Hirai A.;
RT "Transcript levels of tandem-arranged alternative oxidase genes in
RT rice are increased by low temperature.";
RL Gene 203:121-129(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HAYAYUKI; TISSUE=ANTHER;
RA Abe F., Kitashiba H., Kishitani S., Toriyama K.;
RT "Isolation of a cDNA clone encoding the alternative oxidase expressed
RT in rice anthers.";
RL Sex. Plant Reprod. 10:374-375(1997).
DR EMBL; AB004864; BAA28773.1; -
DR EMBL; AB004813; BAA28772.1; -
DR EMBL; AB007452; BAA86963.1; -
DR InterPro; IPR002680; AOX.
DR Pfam; PF01786; AOX; 1.
SQ SEQUENCE 332 AA; 37136 MW; 1A13C511404B60AD CRC64;

Query Match 10.8%; Score 199; DB 10; Length 332;
Best Local Similarity 27.5%; Pred. No. 3.3e-10;
Matches 73; Conservative 36; Mismatches 96; Indels 60; Gaps 10;

QY 62 DDEKVVV-----EESKATSTGTE-----PLEEPNSSSTSAFELWIKLEQGV 108
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 74 DAEKVVVNSWIGJQSKLVREDGTEKMSCFRPMW-----TYTADISDLTKHHV 125
| : : : : : | : : : : : | : : : : : | : : : : : |
QY 109 NVFLTDSV---IKIL---DTLYRDTYAFVLETIARVPYPAFMSVLHM-----YET 155
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 126 PKTLIDKIAVWTVKSRLRPDTIFQRRYGCAMMLETVAAPGVGMLHLRLSRFEG 185
| : : : : : | : : : : : | : : : : : | : : : : : |
QY 156 FGMWRADYLVKVAESNMENHLLIMEELGNSWFDRLAHIATFYFMVLYILS 215
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 186 SGGW-----IRTLLEFAENEMHLMTEMEV-ANPKWYERALVITVQGVFNAYFLGYLLS 239
| : : : : : | : : : : : | : : : : : | : : : : : |
QY 216 PRMAYHSECVESHAYETDYFKL-ASGEELKNMPAPDIAVKYTGDDLYLFDFOFSRT 274
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 240 PKFAHRYVGYLEERAIHSYTEFLKDLGAKIDNVPAPALAIYW----- 283
| : : : : : | : : : : : | : : : : : | : : : : : |
QY 275 PNTRRPVLENLYDVFNIRDEDAH 299
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 284 ---RLPANAATLKDVVTVVRADDAH 305
| : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 13
Q9LQ04 PRELIMINARY; PRT; 318 AA.
AC Q9LQ04;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE F5D14.11 protein.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Liu S.X., Chan A., Yu G., Lee J.M., Lenz C., Pham P., Sakano H.,
RA Toriumi M., Vysotskaya V.S., Chin C., Chou J., Choi E., Chung M.,
RA Gonzalez A., Howing B., Liu A., Vaysberg M., Altafi H., Brooks S.,
RA Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.F.,
RA Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M.,
RA Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
RA Federspiel N.A., Theologis A.;
RT "The sequence of BAC F5D14 from Arabidopsis thaliana chromosome 1.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RT Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC007767; AAF81331.1; -
DR InterPro; IPR002680; AOX.
DR Pfam; PF01786; AOX; 1.
SQ SEQUENCE 318 AA; 36202 MW; F45F0526F86DD5A0 CRC64;

Query Match 10.5%; Score 194.5; DB 10; Length 318;
Best Local Similarity 25.9%; Pred. No. 8.3e-10;
Matches 83; Conservative 50; Mismatches 112; Indels 75; Gaps 17;

QY 16 RPLV--TLRRRAVSYSSHRLHLPLSRLL-----LRNNHVOATILQDEEK 66
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 11 RPLVSSSVSSVSSGLIGGRGH-LISHLP--NVRLLSPTSPVSGNNOPEPDIRAD-GK 66
| : : : : : | : : : : : | : : : : : | : : : : : |
QY 67 VVVEESFKATSTGTEP--LEEPNSSSTSAFELW-----IKLEGVN----- 109
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 67 VI-----STWGIPTPTITKPDGSAMKWCFOQWDSYKRPVSTIDVTKHHPKPSFTK 119
| : : : : : | : : : : : | : : : : : | : : : : : |
QY 110 VFLTDSVIRKILDTLYRDRY-ARFVLETIARVPYPAFMSVLHM-----YETFGWRAD 163
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 120 AVWTQVTKIPQLPFRQRHMCAMMLETVAAPGVGMLHLRLSRFEGSW----- 175
| : : : : : | : : : : : | : : : : : | : : : : : |
QY 164 YLKVHVAESNMENHLLIMEELGNSWFDRLAHIATFYFMVLYILSPRAY 220
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 176 -IKALLLEFAENEMHLMTEIEL-SQPKWYERAIPTVQGVFNAYFLA---YVISPKLAH 230
| : : : : : | : : : : : | : : : : : | : : : : : |
QY 221 HFECEVESHAYETDYFKL-ASGEELKNMPAPDIAVKYTGDDLYLFDFOFSRTPNTR 279
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 231 RTIGYILEERAVNSYTEFLKDLGAKFENSPAPALAIYW-----RL 271
| : : : : : | : : : : : | : : : : : | : : : : : |
QY 280 PVLENLYDVFNIRDEDAH 299
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 272 PKDATLRDVVTVVRADDAH 291
| : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 14
Q9AYP1 PRELIMINARY; PRT; 353 AA.
AC Q9AYP1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Alternative oxidase.
OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
OC Vincet; Catharanthus.
OX NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.

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RA Kiyota S., Sakano K.;  
 RT "Catharantus roseus DNA for alternative oxidase."  
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AB055060; BAB21500.1; -  
 DR InterPro: IPR002680; AOX.  
 DR Pfam: PF01786; AOX; 1.  
 SQ SEQUENCE 353 AA: 40096 MW: 2BED4FCEDB65D00D CRC64;

Query Match 10.5%; Score 193; DB 10; Length 353;  
 Best Local Similarity 23.5%; Pred. No. 1.3e-09;  
 Matches 84; Conservative 53; Mismatches 124; Indels 96; Gaps 15;

QY 7 TGGGTTTISRPVLTTRRAAAYSSSHRLHLPL-----SSRR- 46  
 DB 2 MGRAGTRISRLT---COISPRYFSSAAVRCHEPGLITSGTTFPLHGNPGNGSERT 57  
 QY 47 -----LLRNHHVQATLLDDEKYYVESEFKAETSTGE-----LEPRMSS 92  
 DB 58 ALTWIKLPMRRARSSTAVTVDOKDEKREDKNGVADGENKAVSYGVEAPRLTKE 117  
 QY 93 S-----TSAFETW-----IKLEGVNVELTDSV-----IKIL-----DTLYRDRTYAR 131  
 DB 118 DGVWMTGCFRPEYTKPPTDIELKHHVPVLLDKVAFETVKALRMPDLEFQRYGCR 177  
 QY 132 FVLELTARVYFAFNSVLH-----MYTFGMMRRADYLKHPAESWNEHLLIMEELG 186  
 DB 178 AMLETVAAVPCWVGMLLCHKSLRFEHSGW-----IKALLEAENRMLMTFMEV- 231  
 QY 187 GNSMWFDR---FLAOHIAFFYFMTVFLILSPRAYHFSECVESHAYETYDKFLKASGE 243  
 DB 232 SKRWTERLAVFVGVFNAYFLT--YLASPKLAHRIYGLYEELATHSYSEFLNEIDK 288  
 QY 244 -ELKNRPADIAVKYTGDLFLDEFQTSRTPNTRPIENLYDFVNIRODEAH 299  
 DB 289 GNENPAPALAIIDYW-----QMPDSTLRDVMYVYRADEAH 326

RESULT 15  
 Q8M4M4  
 ID 08M4M4 PRELIMINARY: PRT: 326 AA.  
 AC 08M4M4:  
 DT 01-MAR-2002 (TREMblrel. 20, Created)  
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Putative alternative oxidase.  
 GN AOX.  
 OS Vigna unguiculata (Cowpea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.  
 OX NCBI\_TaxID=3917;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. EPACE-1; TISSUE=LEAF;  
 RA Costa J.H., Hasenratz-Saunders M.P., Jolivet Y., Fernandes de Melo D.,  
 RA Pham-Thi A.T., Silva Lima M., Dizengremel P.;  
 RT "Identification and sequencing of two cDNA clones encoding Vigna  
 RT unguiculata alternative oxidase."  
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AA421015; CAD12835.1; -  
 DR InterPro: IPR002680; AOX.  
 DR Pfam: PF01786; AOX; 1.  
 SQ SEQUENCE 326 AA: 37247 MW: C6268A871E8B8400 CRC64;

Query Match 10.4%; Score 192; DB 10; Length 326;  
 Best Local Similarity 25.8%; Pred. No. 1.5e-09;  
 Matches 85; Conservative 41; Mismatches 121; Indels 82; Gaps 14;

QY 20 TLRSSRAAAYSSSHRLHLPLSS-----RL-----LLRNHRYO 56  
 DB 4 TLVSAARALLGGGRYRHAFTALVEPTROHGGAFCGAFYLRKMSLTLPDKHNSSEK 63  
 QY 57 ATLDDDEKYYVEESF-----KAETSTGTLEPBNMSSSTSAFETW-----IIK 103

DB 64 KNEVDDMTNNAVSISSYWGISRPKVAREDTGE-----WPNMCFPMDTYHSDVSDV 114  
 QY 104 LEQGVNVELTDSV-----IKILDLY-RDRTYARFVLETIRVYFAFMSVLHMYET 155  
 DB 115 TKHHTPKSLTDKVAFRSVKFLRVLSDLVFKERYGCHAMMETIAVGMWGMGLHLKSL 174  
 QY 156 FGWWRADYLKHPAESWNEHLLIMEELGNSMWFDR---FLAOHIAFFYFMTVFLY 212  
 DB 175 RKFGHSGGMITALLLEAENRMLMTWEL-VQPKHIERLLIFTAOGV--FFNAFVFY-Y 230  
 QY 213 ILSPRAYHFSECVESHAYETYDKFLKA--SGEELKNRPADIAVKYTGDLFLDEFQ 270  
 DB 231 LLSPKAARFVGYLSEEAIVISYTOHLEAIFSG-KVENPAPALAIIDYW----- 277  
 QY 271 TSRTPTRRPIENLYDFVNIRODEAH 299  
 DB 278 -----RLPKDATLKDVMYVYRADEAH 299

Search completed: February 2, 2003, 22:47:49  
 Job time : 89 secs

